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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.



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UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy¹⁻⁶⁶. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (<http://www.ncbi.nlm.nih.gov>) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals⁶⁷. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics⁶⁸ blood heam analysis^{69,70} etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification⁷¹, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity^{72,73}. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wantonly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECULAR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:
Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctagtaga
 atgaatctgaggagggttctcagtagataaagcaacccttaccggatttttcgccttccactttatctcccatttatcattgcagccctt
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac
 ccctactacacatatcaaagatatcctaggagctctactattaatttaaccctcatgcttctagtcctattctcaccggacctgcttggag
 5 accagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct
 ccgatcaattcctaacaaactaggagg”.

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as ‘mcb398’ and ‘mcb869’ because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398
 10 to 869 of *Antelope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3’ end are highly conserved amongst a vast range of animal
 15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate
 20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers ‘mcb398’ and ‘mcb869’ invented by the applicants fulfill the objectives of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using ‘BLAST software’⁷³, it indicates identity of the family, genus or species of the analyzed
 30 material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers ‘mcb398’ and ‘mcb869’. The complete procedure involved in the *analyses* (the word, ‘analyses’ should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

5 **Figure 1a.** Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures⁷⁴. The DNA obtained was amplified using the primers
10 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were
15 sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in *analyses*. The sequence (328 bp)
20 revealed from 'adil.flesh' was subjected to homology search in *nr* (i.e. non-redundant) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis
25 revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of
30 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

10 Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

20 **Figure 4.** Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species
Symbol (^sP,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol (\overline{P} , S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

5 **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species
10 listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements
15 of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170)
25 registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera paurdus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in
30 Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark:

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard '*Panthera pardus*' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard '*Panthera pardus*' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis⁷⁵; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-wise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software *PHYLIP* (3.5).

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in *nr* database of NCBI. It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

Table 12. Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions⁷⁵. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI¹⁻⁶⁵. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small

20 fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software *CLUSTAL X* (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctagtaga
 5 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgccttcactttatcctcccattatcattgcagccctt
 accatagtagacactactgtttctccacgaaacaggatccaacaacccccacaggaatctcatcagacgcagacaaaaatccaticcac
 ccctactacactatcaaagatatcctaggagctctactattaatttaaacctcatgcttctagtctattctcaccggacctgcttgag
 accagacaactataaccagcaaaccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcgaatcct
 ccgatcaattcctaacaaactaggagg

10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked
 15 with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

| Primers name | Sequence (5'-3') |
|--------------|------------------------------|
| 20 'mcb398' | “TACCATGAGGACAAATATCATTCTG” |
| 'mcb869' | “CCTCCTAGTTTGTTAGGGATTGATCG” |

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the
 25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of
 30 match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template):

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were

5 *Eumeces egregious* and *Equus ainus*. *Eumeces egregious* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S

10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataaggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed

15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869',

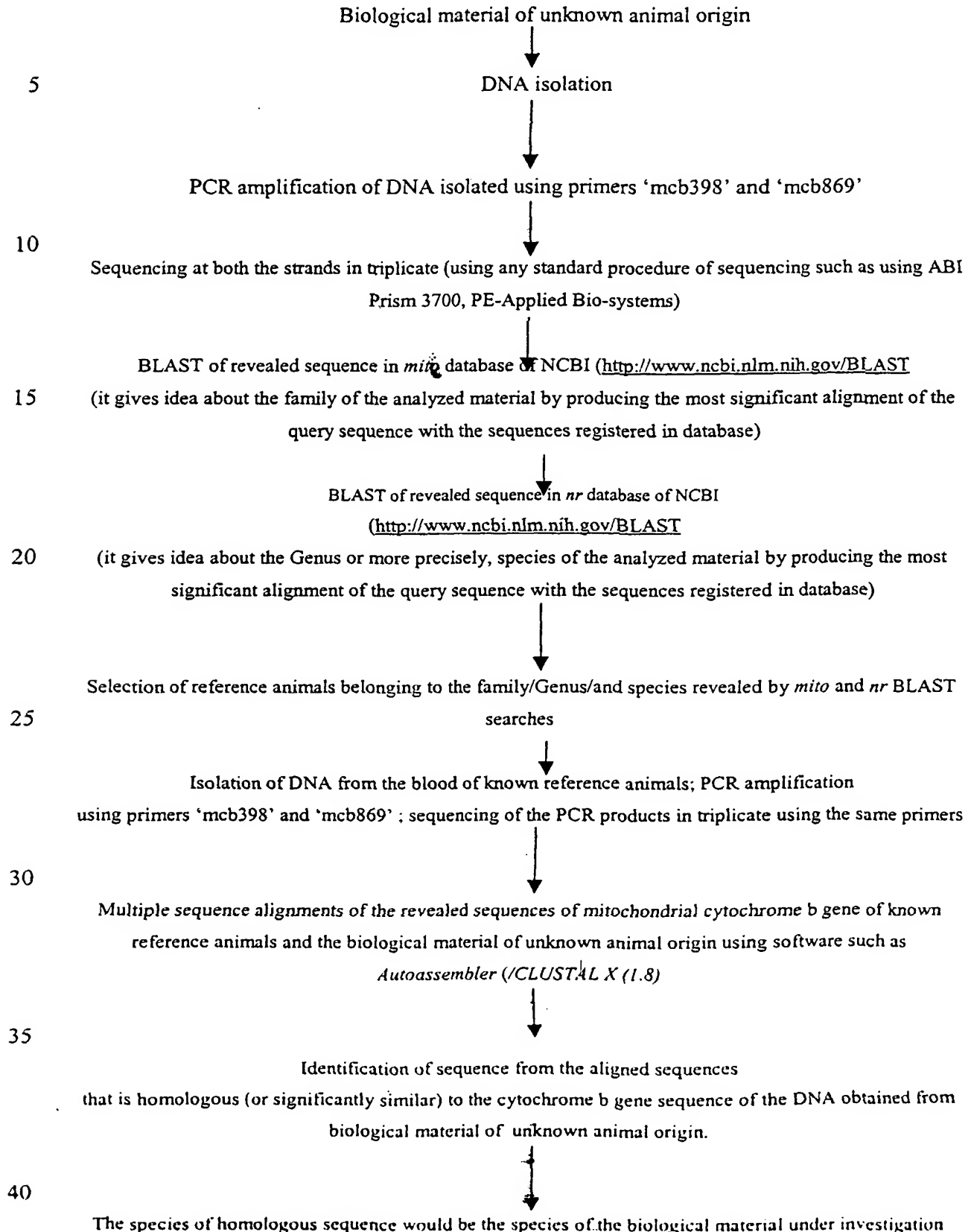
20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb

25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



Examples

Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading
5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources¹⁻⁶⁵. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*
10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species
15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated from any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using
20 software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are
30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcggtacaaacctagtaga
 atgaatctgaggagggtctcagtagataaagcaacccttaccgattttcgccttcactttatcctccatttatcattgcagccctt
 accatagtacactactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaaattccattccac
 ccctactacactatcaaagatactcctaggagctctactattaatttaacccctcatgcttctagtctctattctcaccggacctgcttgag
 5 accagacaactatacaccagcaaaccacttaatacacccccacatatcaagcccgatgatacttctatttgcatagcgaatcct
 ccgatcaattcctaacaaactaggagg”

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The t_m (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer *would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.*
5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

8. The sequences of the universal primers invented are as follows:

| Primers name | Sequence (5'-3') |
|--------------|-----------------------------|
| 'mcb398' | "TACCATGAGGACAAATATCATTCTG" |
| 'mcb869' | "CCTCCTAGTTTGTAGGGATTGATCG" |

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 μ l reaction volume containing approximately 20 ng of template DNA, 100 μ M each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

Example 4:

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X* (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'ctagtagaatgaatctgaggagg⁵ and AFR= 5'tatgcaaataaggaagtatcattc³.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869', respectively, were higher than the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

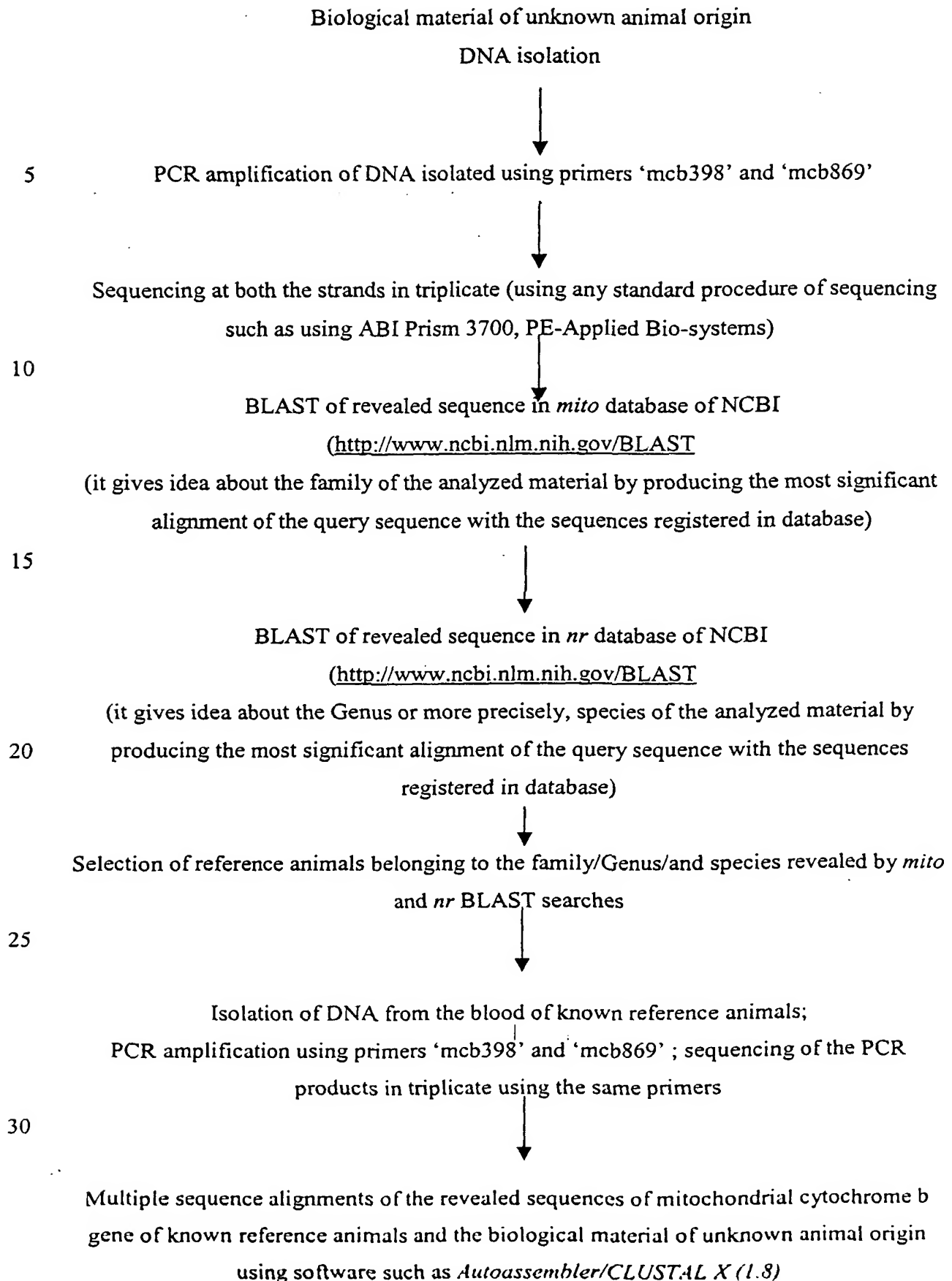
(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:





Identification of sequence from the aligned sequences
that is homologous (or significantly similar) to the cytochrome b gene sequence of the
5 DNA obtained from biological material of
unknown animal origin.



10 The species of homologous sequence would be the species of the biological material under
investigation



Application of the above information for the objectives mentioned in columns 7-13 under
sub-heading 'Objective of invention' of heading 'Summary of invention'

15 **Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we
investigated a case of forensic identification submitted at our laboratory to seek scientific
opinion on animal hunting evidence. In this case, we received the half burned remains of
20 an unknown animal, confiscated by the crime investigation agencies. The DNA was
isolated from the above material following standard methods⁷⁴ and subjected to PCR
amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869').
Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of
template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit
25 of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer
(10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an
initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C
for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step
at 35th cycles was held for 10 min.

30 The PCR products obtained were sequenced in automated work station (ABI Prism 3700,
PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in
Figure 1a) was blasted against *mito* databases of NCBI using BLAST program⁷³. The most
significant alignment (bits Value 365, E value e^{-101}) of this sequence was produced with
the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e^{-170}) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-wise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-wise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source (99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Panthera pardus*) species. The step-wise procedure involved in above analysis is illustrated in Figure 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

| SN. Code | Name | NCBI accession # | [†] P,S/F | [‡] P,S/R |
|----------------|---------------------------------------|------------------------|--------------------|--------------------|
| 1 aep.mel | <i>Aepyceros melampus</i> | AF036289 ¹ | 97, 60 | 94, 62 |
| 2 ore.ore | <i>Oreotragus oreotragus</i> | AF036283 ¹ | 88, 52 | 94, 62 |
| 3 add.nas | <i>Addax nasomaculatus</i> | AF034722 ² | 97, 60 | 95, 66 |
| 4 ory.dam | <i>Oryx damah</i> | AJ222685 ¹ | 90, 58 | 95, 66 |
| 5 hip.equ | <i>Hippotragus equinus</i> | AF022060 ³ | 98, 63 | 85, 55 |
| 6 alc.bus | <i>Alcelaphus buselaphus</i> | AJ222681 ¹ | 97, 60 | 98, 68 |
| 7 sig.lic | <i>Sigmoceros lichtensteinii</i> | AF034967 ⁴ | 97, 60 | 98, 68 |
| 8 bea.hun | <i>Beatragus hunteri</i> | AF034968 ⁴ | 97, 60 | 94, 62 |
| 9 dam.lun | <i>Damaliscus lunatus</i> | AF016635 ³ | 97, 60 | 77, 55 |
| 10 con.tau | <i>Connochaetes taurinus</i> | AF016638 ³ | 82, 56 | 93, 62 |
| 11 bis.bon | <i>Bison bonasus</i> | Y15005 ⁵ | 90, 58 | 87, 63 |
| 12 bos.gru | <i>Bos grunniens</i> * | AF091631 ⁶ | 90, 58 | 94, 62 |
| 13 bos.tra | <i>Bos tragocamelus</i> * | AJ222679 ¹ | 90, 58 | 95, 66 |
| 14 buba.bub | <i>Bubalus bubalis</i> * | D34637 ⁷ | 97, 60 | 93, 64 |
| 15 bub.min | <i>Bubalus mindorensis</i> | D82895 ⁸ | 97, 60 | 87, 62 |
| 16 tra.ang | <i>Tragelaphus angasii</i> | AF091633 ⁶ | 97, 60 | 87, 63 |
| 17 tra.eur | <i>Tragelaphus eurycerus</i> | AF036276 ¹ | 90, 58 | 97, 64 |
| 18 nem.cau | <i>Nemorhaedus caudatus</i> * | U17861 ⁹ | 95, 61 | 93, 59 |
| 19 pse.nay | <i>Pseudois nayaur</i> | AF034732 ² | 89, 55 | 89, 59 |
| 20 amm.ler | <i>Ammotragus lervia</i> | AF034731 ² | 94, 58 | 97, 63 |
| 21 cap.fal | <i>Capra falconeri</i> * | D84202 ¹⁰ | 98, 63 | 95, 66 |
| 22 cap.ibe | <i>Capra ibex</i> * | AF034735 ² | 98, 63 | 89, 58 |
| 23 hem.jem | <i>Hemitragus jemlahicus</i> * | AF034733 ² | 95, 61 | 90, 61 |
| 24 rup.pyr | <i>Rupicapra pyrenaica</i> | AF034726 ² | 95, 61 | 89, 59 |
| 25 rup.rup | <i>Rupicapra rupicapra</i> | AF034725 ² | 95, 61 | 94, 64 |
| 26 pan.hod | <i>Pantholops hodgsoni</i> | AF034724 ² | 98, 63 | 95, 66 |
| 27 bud.tax.tax | <i>Budorcas taxicolor taxicolor</i> * | U17868 ⁹ | 90, 58 | 95, 66 |
| 28 ovi.ammm | <i>Ovis ammon</i> * | AF034727 ² | 98, 63 | 97, 64 |
| 29 ovi.vig | <i>Ovis vignei</i> * | AF034729 ² | 98, 63 | 97, 64 |
| 30 cap.cri | <i>Capreolus crispus</i> * | AJ304502 ¹¹ | 98, 63 | 94, 63 |
| 31 ovi.mos | <i>Ovibos moschatus</i> | U17862 ⁹ | 98, 63 | 92, 61 |
| 32 ore.ame | <i>Oreamnos americanus</i> | AF190632 ¹² | 98, 63 | 94, 62 |
| 33 cep.dor | <i>Cephalophus dorsalis</i> | AF091634 ⁶ | 97, 58 | 90, 61 |
| 34 cep.max | <i>Cephalophus maxwellii</i> | AF096629 ¹³ | 97, 60 | 88, 53 |
| 35 alc.alc | <i>Alces alces</i> | AJ000026 ¹⁴ | 95, 61 | 93, 59 |
| 36 hyd.ine | <i>Hydropotes inermis</i> | AJ000028 ¹⁴ | 97, 60 | 90, 63 |
| 37 mun.mun | <i>Muntiacus muntjak</i> * | AF042713 ¹⁵ | 90, 58 | 93, 64 |
| 38 cer.ele.kan | <i>Cervus elaphus kansuensis</i> * | AB021098 ¹⁶ | 98, 63 | 82, 59 |
| 39 cer.ele.xan | <i>Cervus elaphus xanthopygus</i> * | AB021097 ¹⁶ | 98, 63 | 82, 59 |
| 40 cer.ele.can | <i>Cervus elaphus canadensis</i> * | AB021096 ¹⁶ | 98, 63 | 90, 61 |
| 41 cer.nip.ce | <i>Cervus nippon centralis</i> | AB021094 ¹⁶ | 98, 63 | 90, 61 |
| 42 cer.nip.ye | <i>Cervus nippon yesoensis</i> | AB021095 ¹⁶ | 98, 63 | 90, 61 |
| 43 cer.nip.ke | <i>Cervus nippon keramuc</i> | AB021091 ¹⁶ | 98, 63 | 90, 61 |

| | | | | | |
|----|------------|------------------------------------|-------------------------|--------|--------|
| 44 | cer.nip.pu | <i>Cervus nippon pulchellus</i> | AB021090 ¹⁶ | 98, 63 | 90, 61 |
| 45 | cer.nip.ni | <i>Cervus nippon nippon</i> | AB021093 ¹⁶ | 98, 63 | 90, 61 |
| 46 | cer.ela.sc | <i>Cervus elaphus scoticus</i> | AB021099 ¹⁶ | 98, 63 | 90, 61 |
| 47 | cer.dam | <i>Cervus dama</i> | AJ000022 ¹⁴ | 98, 63 | 88, 53 |
| 48 | ran.tar | <i>Rangifer tarandus</i> | AJ000029 ¹⁴ | 98, 63 | 89, 57 |
| 49 | mos.fus | <i>Moschus fuscus</i> * | AF026883 ¹⁷ | 90, 59 | 90, 61 |
| 50 | mos.leu | <i>Moschus leucogaster</i> * | AF026889 ¹⁷ | 90, 59 | 90, 61 |
| 51 | mos.chr | <i>Moschus chrysogaster</i> * | AF026887 ¹⁷ | 90, 59 | 90, 61 |
| 52 | mos.ber | <i>Moschus berezovskii</i> * | AF026886 ¹⁷ | 90, 59 | 90, 61 |
| 53 | mos.mos | <i>Moschus moschiferus</i> * | AF026883 ¹⁷ | 90, 59 | 92, 61 |
| 54 | kob.ell | <i>Kobus ellipsiprymnus</i> | AF022059 ³ | 91, 61 | 95, 66 |
| 55 | kob.meg | <i>Kobus megaceros</i> | AJ222686 ¹ | 91, 61 | 83, 56 |
| 56 | red.aru | <i>Redunca arundinum</i> | AF096628 ¹³ | 91, 61 | 94, 62 |
| 57 | red.ful | <i>Redunca fulvorufula</i> | AF036284 ¹ | 89, 57 | 94, 62 |
| 58 | neo.mos | <i>Neotragus moschatus</i> | AJ222683 ¹ | 89, 57 | 94, 62 |
| 59 | pel.cap | <i>Pelea capreolus</i> | AF022055 ³ | 91, 61 | 90, 61 |
| 60 | ant.cer | <i>Antilope cervicapra</i> * | AF022058 ³ | 82, 56 | 93, 64 |
| 61 | sai.tat | <i>Saiga tatarica</i> | AF064487 ¹⁸ | 91, 61 | 92, 61 |
| 62 | gaz.dam | <i>Gazella dama</i> | AF025954 ³ | 91, 61 | 92, 61 |
| 63 | our.our | <i>Ourebia ourebi</i> | AF036288 ¹ | 82, 56 | 82, 59 |
| 64 | gaz.gaz | <i>Gazella gazella</i> * | AJ222682 ¹ | 91, 61 | 89, 57 |
| 65 | rap.mel | <i>Raphicerus melanotis</i> | AF022053 ³ | 81, 54 | 80, 50 |
| 66 | mad.kir | <i>Madoqua kirkii</i> | AF022070 ³ | 90, 58 | 97, 65 |
| 67 | ant.ame | <i>Antilocapra americana</i> | AF091629 ⁶ | 98, 63 | 98, 68 |
| 68 | tra.jav | <i>Tragulus javanicus</i> * | D32189 ¹⁹ | 86, 57 | 86, 59 |
| 69 | tra.nap | <i>Tragulus napu</i> * | X56288 ²⁰ | 81, 52 | 93, 58 |
| 70 | bal.acu | <i>Balaenoptera acutorostrata</i> | X75753 ²¹ | 89, 56 | 97, 61 |
| 71 | bal.bon | <i>Balaenoptera bonaerensis</i> | X75581 ²¹ | 89, 56 | 93, 59 |
| 72 | bal.bor | <i>Balaenoptera borealis</i> * | X75582 ²¹ | 89, 56 | 93, 59 |
| 73 | bal.edi | <i>Balaenoptera edeni</i> | X75583 ²¹ | 89, 56 | 88, 54 |
| 74 | esc.rob | <i>Eschrichtius robustus</i> * | X75585 ²¹ | 97, 61 | 86, 57 |
| 75 | bal.mus | <i>Balaenoptera musculus</i> * | NC_001601 ²² | 97, 57 | 93, 59 |
| 76 | meg.nov | <i>Megaptera novaeangliae</i> * | X75584 ²¹ | 97, 61 | 94, 63 |
| 77 | bal.phy | <i>Balaenoptera physalus</i> * | NC_001321 ²³ | 97, 57 | 94, 63 |
| 78 | cap.mar | <i>Caperea marginata</i> | X75586 ²¹ | 93, 55 | 91, 53 |
| 79 | cep.com | <i>Cephalorhynchus commersonii</i> | AF084073 ²⁴ | 85, 51 | 88, 55 |
| 80 | cep.eut | <i>Cephalorhynchus eutropia</i> * | AF084072 ²⁴ | 85, 51 | 92, 59 |
| 81 | lag.obl | <i>Lagenorhynchus obliquidens</i> | AF084067 ²⁴ | 94, 59 | 92, 59 |
| 82 | cep.hec | <i>Cephalorhynchus heavisidii</i> | AF084070 ²⁴ | 89, 56 | 97, 63 |
| 83 | cep.hec | <i>cephalorhynchus hectori</i> * | AF084071 ²⁴ | 89, 56 | 92, 59 |
| 84 | lag.aus | <i>Lagenorhynchus australis</i> | AF084069 ²⁴ | 86, 54 | 92, 59 |
| 85 | lag.cru | <i>Lagenorhynchus cruciger</i> | AF084068 ²⁴ | 86, 54 | 92, 59 |
| 86 | lag.obs | <i>Lagenorhynchus obscurus</i> | AF084066 ²⁴ | 86, 54 | 92, 59 |
| 87 | lis.bor | <i>Lissodelphis borealis</i> | AF084064 ²⁴ | 85, 51 | 92, 59 |
| 88 | lis.per | <i>Lissodelphis peronii</i> | AF084065 ²⁴ | 86, 54 | 92, 59 |
| 89 | glo.mac | <i>Globicephala macrorhynchus</i> | AF084055 ²⁴ | 94, 59 | 88, 55 |
| 90 | glo.mel | <i>Globicephala melas</i> | AF084056 ²⁴ | 94, 59 | 88, 55 |
| 91 | fer.att | <i>Feresa attenuata</i> * | AF084052 ²⁴ | 94, 59 | 92, 59 |

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|-----|------------|------------------------------------|-------------------------|--------|--------|
| 92 | pep.ele | <i>Peponocephala electra</i> * | AF084053 ²⁴ | 94, 59 | 88, 55 |
| 93 | gra.gri | <i>Grampus griseus</i> | AF084059 ²⁴ | 97, 61 | 89, 59 |
| 94 | pse.cra | <i>Pseudorca crassidens</i> * | AF084057 ²⁴ | 94, 59 | 92, 59 |
| 95 | lag.acu | <i>Lagenorhynchus acutus</i> | AF084075 ²⁴ | 98, 63 | 89, 59 |
| 96 | orci.bre | <i>Orcinus orca</i> | AF084061 ²⁴ | 86, 57 | 82, 52 |
| 97 | orca.bre | <i>Orcaella brevirostris</i> | AF084063 ²⁴ | 86, 57 | 91, 54 |
| 98 | del.cap | <i>Delphinus capensis</i> | AF084087 ²⁴ | 96, 54 | 97, 63 |
| 99 | del.tro | <i>Delphinus tropicalis</i> | AF084088 ²⁴ | 97, 57 | 97, 63 |
| 100 | del.del | <i>Delphinus delphis</i> | AF084085 ²⁴ | 97, 57 | 97, 63 |
| 101 | sten.cly | <i>Stenella clymene</i> | AF084083 ²⁴ | 97, 57 | 97, 63 |
| 102 | sten.coe | <i>Stenella coeruleoalba</i> | AF084082 ²⁴ | 97, 57 | 97, 66 |
| 103 | tur.adu | <i>Tursiops aduncus</i> | AF084092 ²⁴ | 97, 57 | 97, 63 |
| 104 | sten.fro | <i>Stenella frontalis</i> | AF084090 ²⁴ | 97, 57 | 97, 63 |
| 105 | saus.chi | <i>Sousa chinensis</i> | AF084080 ²⁴ | 97, 57 | 88, 59 |
| 106 | sten.lon | <i>Stenella longirostris</i> | AF084103 ²⁴ | 97, 61 | 97, 63 |
| 107 | turs.tru | <i>Tursiops truncatus</i> | AF084095 ²⁴ | 97, 57 | 96, 59 |
| 108 | lage.alb | <i>Lagenorhynchus alborostris</i> | AF084074 ²⁴ | 97, 61 | 97, 66 |
| 109 | sten.bre | <i>Steno bredanensis</i> | AF084077 ²⁴ | 97, 61 | 94, 64 |
| 110 | sota.flu | <i>Sotalia fluviatilis</i> | AF304067 ²⁵ | 97, 61 | 97, 63 |
| 111 | del.leu | <i>Delphinapterus leucas</i> | U72037 ²⁶ | 97, 61 | 95, 66 |
| 112 | mono.mon | <i>Monodon monoceros</i> | U72038 ²⁶ | 97, 61 | 95, 66 |
| 113 | plat.gan | <i>Platanista gangetica</i> * | AF304070 ²⁵ | 97, 61 | 86, 59 |
| 114 | plat.min | <i>Platanista minor</i> * | X92543 ²⁷ | 97, 61 | 86, 59 |
| 115 | kogi.bre | <i>Kogia breviceps</i> | U72040 ²⁶ | 97, 59 | 90, 63 |
| 116 | kogi.sim | <i>Kogia simus</i> | AF304072 ²⁵ | 96, 55 | 92, 63 |
| 117 | phys.cat | <i>Physeter catodon</i> | AF304073 ²⁵ | 97, 57 | 80, 58 |
| 118 | lipo.vex | <i>Lipotes vexillifer</i> * | AF304071 ²⁵ | 89, 56 | 83, 53 |
| 119 | phoc.sin | <i>phocoena sinus</i> | AF084051 ²⁴ | 87, 49 | 92, 62 |
| 120 | bera.bai | <i>Berardius bairdii</i> | X92541 ²⁷ | 96, 55 | 90, 59 |
| 121 | ziph.car | <i>Ziphius cavirostris</i> | X92540 ²⁷ | 97, 61 | 89, 57 |
| 122 | meso.eur | <i>Mesoplodon europaeus</i> | X92537 ²⁷ | 97, 57 | 90, 61 |
| 123 | meso.bid | <i>Mesoplodon bidens</i> | X92538 ²⁷ | 97, 61 | 92, 61 |
| 124 | meso.den | <i>Mesoplodon densirostris</i> | X92536 ²⁷ | 91, 61 | 94, 63 |
| 125 | hype.amp | <i>Hyperoodon ampullatus</i> * | X92539 ²⁷ | 97, 61 | 90, 65 |
| 126 | meso.per | <i>Mesoplodon peruvianus</i> | AF304074 ²⁵ | 97, 61 | 86, 58 |
| 127 | pont.bla | <i>Pontoporia blainvillei</i> | AF304069 ²⁵ | 92, 59 | 88, 55 |
| 128 | hipp.amp | <i>Hippopotamus amphibius</i> | Y08813 ²⁹ | 92, 58 | 95, 66 |
| 129 | hex.lib | <i>Hexaprotodon liberiensis</i> | Y08814 ²⁹ | 98, 63 | 97, 66 |
| 130 | rhin.son | <i>Rhinoceros sondaicus</i> * | AJ245725 ¹⁰ | 90, 59 | 87, 61 |
| 131 | cera | <i>Ceratotherium simum</i> | NC_001808 ¹² | 90, 59 | 90, 63 |
| 132 | dic.sum | <i>Dicerorhinus sumatrensis</i> | AJ245723 ¹⁰ | 90, 59 | 86, 57 |
| 133 | equu | <i>Equus asinus</i> | NC_001788 ¹¹ | 91, 61 | 73, 51 |
| 134 | baby.bab | <i>Babyrousa babyrussa</i> | Z50106 ¹¹ | 89, 56 | 85, 56 |
| 135 | phac.afri | <i>Phacochoerus africanus</i> | Z50090 ¹¹ | 90, 59 | 87, 54 |
| 136 | sus.scr.ew | <i>Sus scrofa haplotype EWBj</i> * | AF136549 ¹⁴ | 97, 57 | 83, 54 |
| 137 | sus.bar | <i>Sus barbatus</i> | Z50107 ¹¹ | 97, 57 | 85, 55 |
| 138 | lama.gla | <i>Lama glama</i> | U06429 ¹¹ | 89, 55 | 85, 53 |
| 139 | lama.gua | <i>Lama guanicoe</i> | Y08812 ²⁹ | 88, 54 | 86, 57 |

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|----------------|---------------------------------|-------------------------|--------|--------|
| 140 vic.vic | <i>Vicugna vicugna</i> | U06430 ³⁵ | 89, 55 | 85, 53 |
| 141 cam.bac | <i>Camelus bactrianus</i> | U06427 ³⁵ | 94, 58 | 86, 58 |
| 142 arc.for | <i>Arctocepalus forsteri</i> | XS2293 ³⁶ | 97, 60 | 87, 64 |
| 143 arc.gaz | <i>Arctocepalus gazella</i> | X82292 ³⁶ | 94, 58 | 87, 64 |
| 144 eum.jub | <i>Eumetopias jubatus</i> | X82311 ³⁶ | 97, 57 | 86, 57 |
| 145 zal.cal | <i>Zalophus californianus</i> | X82310 ³⁶ | 89, 55 | 86, 57 |
| 146 odo.ros | <i>Odobenus rosmarus</i> | X82299 ³⁶ | 91, 61 | 81, 52 |
| 147 pho.vit | <i>Phoca vitulina</i> | X82306 ³⁶ | 90, 58 | 87, 64 |
| 148 pho.fascia | <i>Phoca fasciata</i> | X82302 ³⁶ | 98, 63 | 95, 66 |
| 149 pho.gro | <i>Phoca groenlandica</i> | X82303 ³⁶ | 92, 59 | 90, 61 |
| 150 cys.cri | <i>Cystophora cristata</i> | X82294 ³⁶ | 89, 56 | 87, 64 |
| 151 hyd.lep | <i>Hydrurga leptonyx</i> | X82297 ³⁶ | 89, 55 | 82, 54 |
| 152 lep.wed | <i>Leptonychotes weddelli</i> | X72005 ³⁷ | 98, 63 | 91, 66 |
| 153 mir.leo | <i>Mirounga leonina</i> | X82298 ³⁶ | 89, 55 | 82, 59 |
| 154 eri.bar | <i>Erignathus barbatus</i> | X82295 ³⁶ | 89, 56 | 87, 63 |
| 155 mon.sch | <i>Monachus schauinslandi</i> | X72209 ³⁷ | 91, 61 | 87, 60 |
| 156 hela.mal | <i>Helarctos malayanus</i> * | U18899 ³⁸ | 84, 54 | 90, 63 |
| 157 sel.thi | <i>Selenarctos thibetanus</i> * | AB020910 ³⁹ | 89, 57 | 87, 64 |
| 158 ail.ful | <i>Ailurus fulgens</i> * | X94919 ⁴⁰ | 93, 55 | 87, 64 |
| 159 fel | <i>Felis catus</i> | NC_001700 ⁴¹ | 85, 56 | 90, 63 |
| 160 can | <i>Canis familiaris</i> | NC_002008 ⁴² | 98, 58 | 84, 54 |
| 161 tal | <i>Talpa europaea</i> | NC_002391 ⁴³ | 81, 50 | 92, 57 |
| 162 gla.sab | <i>Glaucornys sabrinus</i> | AF011738 ⁴⁴ | 90, 59 | 82, 54 |
| 163 gla.vol | <i>Glaucornys volans</i> | AB030261 ⁴⁵ | 90, 59 | 87, 60 |
| 164 hyl.pha | <i>Hylomys phayrei</i> * | AB030259 ⁴⁵ | 91, 61 | 81, 50 |
| 165 pet.set | <i>Petionomys setosus</i> * | AB030260 ⁴⁵ | 91, 61 | 81, 50 |
| 166 bel.pea | <i>Belomys pearsonii</i> * | AB030262 ⁴⁵ | 91, 61 | 87, 64 |
| 167 pte.mom | <i>Pteromys momonga</i> * | AB030263 ⁴⁵ | 97, 61 | 90, 63 |
| 168 gala.demi | <i>Galagoides demidoff</i> | AF271411 ⁴⁶ | 97, 58 | 87, 64 |
| 169 pero.pot | <i>Perodicticus potto</i> | AF271413 ⁴⁶ | 97, 60 | 87, 63 |
| 170 gala.mat | <i>Galago matschiei</i> | AF271409 ⁴⁶ | 97, 60 | 90, 61 |
| 171 gala.moh | <i>Galago moholi</i> | AF271410 ⁴⁶ | 97, 57 | 95, 66 |
| 172 oto.gar | <i>Otolemur garnettii</i> | AF271412 ⁴⁶ | 92, 58 | 87, 60 |
| 173 lor.tar | <i>Loris tardigradus</i> * | US3581 ⁴⁷ | 97, 60 | 93, 59 |
| 174 nyc.cou | <i>Nycticebus coucang</i> * | US3580 ⁴⁷ | 97, 60 | 95, 66 |
| 175 mus | <i>Mus musculus</i> | NC_001569 ⁴⁸ | 97, 60 | 86, 59 |
| 176 gor | <i>Gorilla gorilla</i> | NC_001645 ⁴⁹ | 89, 57 | 80, 58 |
| 177 homo | <i>Homo sapiens sapiens</i> | NC_001807 ⁵⁰ | 96, 55 | 84, 64 |
| 178 dug.dug | <i>Dugong dugong</i> * | U07564 ⁵¹ | 97, 60 | 89, 59 |
| 179 ele.max | <i>Elephas maximus</i> * | AB002412 ⁵² | 97, 60 | 76, 57 |
| 180 afr.con | <i>Afropavo congensis</i> | AF013760 ⁵³ | 97, 58 | 87, 63 |
| 181 pavo.mut | <i>Pavo muticus</i> * | AF013763 ⁵³ | 97, 57 | 87, 63 |
| 182 tra.bly | <i>Tragopan blythii</i> * | AF200722 ⁵⁴ | 89, 55 | 85, 57 |
| 183 tra.sat | <i>Tragopan satyra</i> * | AF229837 ⁵⁴ | 89, 55 | 86, 61 |
| 184 tra.cob | <i>Tragopan caboti</i> | AF200723 ⁵⁴ | 89, 55 | 86, 61 |
| 185 tra.tem | <i>Tragopan temminckii</i> * | AF023802 ⁵⁵ | 89, 55 | 81, 56 |
| 186 arg.arg | <i>Argusianus argus</i> | AF013761 ⁵⁵ | 89, 55 | 87, 63 |
| 187 cat.wal | <i>Catrus wallichii</i> * | AF028792 ⁵⁵ | 88, 54 | 85, 57 |

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|-----|------------|------------------------------------|-------------------------|--------|--------|
| 188 | cro.cro | <i>Crossoptilon crossoptilon</i> * | AF028794 ⁵¹ | 89, 55 | 85, 57 |
| 189 | sym.ree | <i>Syrnaticus reevesi</i> * | AF028801 ⁵¹ | 89, 55 | 85, 57 |
| 190 | bam.tho | <i>Bambusicola thoracica</i> * | AF028790 ⁵¹ | 80, 48 | 94, 64 |
| 191 | fra.fra | <i>Francolinus francolinus</i> | AF013762 ⁵³ | 97, 58 | 86, 61 |
| 192 | ith.cru | <i>Ithaginis cruentus</i> * | AF068193 ⁵³ | 98, 63 | 85, 57 |
| 193 | ant.par | <i>Anthropoides paradisca</i> | U27557 ⁵⁶ | 85, 56 | 82, 58 |
| 194 | ant.vir | <i>Anthropoides virgo</i> | U27545 ⁵⁶ | 84, 54 | 82, 52 |
| 195 | gru.ant.an | <i>Grus antigone antigone</i> | U11060 ⁵⁷ | 90, 53 | 87, 63 |
| 196 | gru.ant.gi | <i>Grus antigone gillae</i> | U11064 ⁵⁷ | 90, 53 | 87, 63 |
| 197 | gru.any.sh | <i>Grus antigone sharpei</i> | U11061 ⁵⁷ | 90, 53 | 87, 63 |
| 198 | gru.leu | <i>Grus leucogeranus</i> * | U27549 ⁵⁶ | 90, 53 | 87, 63 |
| 199 | gru.can.pr | <i>Grus canadensis pratensis</i> | U27553 ⁵⁶ | 97, 60 | 87, 63 |
| 200 | gru.can.ro | <i>Grus canadensis rowani</i> | U27552 ⁵⁶ | 97, 60 | 87, 63 |
| 201 | gru.can.ta | <i>Grus canadensis tabida</i> | U27551 ⁵⁶ | 98, 63 | 87, 63 |
| 202 | gru.can.ca | <i>Grus canadensis canadensis</i> | U27554 ⁵⁶ | 97, 61 | 87, 63 |
| 203 | gru.ame | <i>Grus americana</i> | U27555 ⁵⁶ | 90, 53 | 87, 63 |
| 204 | gru.gru | <i>Grus grus</i> | U27546 ⁵⁶ | 89, 54 | 87, 63 |
| 205 | gru.mon | <i>Grus monacha</i> * | U27548 ⁵⁶ | 90, 53 | 87, 63 |
| 206 | gru.nig | <i>Grus nigricollis</i> * | U27547 ⁵⁶ | 90, 53 | 87, 63 |
| 207 | gru.jap | <i>Grus japonensis</i> | U27550 ⁵⁶ | 81, 54 | 87, 63 |
| 208 | cic.boy | <i>Ciconia boyciana</i> * | NC_002196 ⁵⁸ | 94, 58 | 79, 60 |
| 209 | rhe.ame | <i>Rhea americana</i> | AF090339 ⁵⁹ | 93, 63 | 79, 60 |
| 210 | ant.alb | <i>Anthracoceros albirostris</i> * | U89190 ⁶⁰ | 97, 61 | 86, 59 |
| 211 | fal.fam | <i>Falco femoralis</i> | U83310 ⁶¹ | 97, 61 | 86, 60 |
| 212 | fal.ver | <i>Falco verpertinus</i> | U83311 ⁶¹ | 97, 61 | 85, 57 |
| 213 | fal.par | <i>Falco peregrinus</i> * | U83307 ⁶¹ | 97, 61 | 84, 52 |
| 214 | fal.spa | <i>Falco sparverius</i> | U83306 ⁶¹ | 92, 59 | 80, 51 |
| 215 | ayt.ame | <i>Aythya americana</i> | NC_000877 ⁶² | 98, 63 | 94, 62 |
| 216 | smi.sha | <i>Smithornis sharpei</i> | NC_000879 ⁵⁹ | 97, 53 | 90, 61 |
| 217 | vid.cha | <i>Vidua chalybeata</i> | NC_000880 ⁵⁹ | 97, 60 | 87, 64 |
| 218 | chry.pic | <i>Chrysemys picta</i> | NC_002073 ⁶³ | 89, 56 | 86, 57 |
| 219 | emy.orb.ku | <i>Emys orbicularis</i> | AJ131425 ⁶⁴ | 90, 59 | 94, 63 |
| 220 | che.mud | <i>Chelonia mydas</i> * | AB012104 ⁶⁵ | 90, 58 | 94, 63 |
| 221 | eum.egr | <i>Eumeces egregius</i> | AB016606 ⁶⁵ | 86, 55 | 73, 51 |

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene of 221 animal species

| PRIMER 'mcb393' | TACCATGAGGACAAATATCATTCTG | |
|-----------------|---|----|
| | | |
| aep.mel | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCTCTCAGCAA | 60 |
| ore.ore | TTCCCTGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAATCTCTCTCAGCAA | 60 |
| add.nas | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| ory.dam | TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| hip.equ | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| alc.bus | TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| sig.lic | TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| bea.hun | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| dam.lun | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCCTAACCCTCTCTCTCAGCAA | 60 |
| con.tau | TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| amm.ler | TGCCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| pse.nay | TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| cap.ibe | TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| hem.jem | TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| cap.fal | TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| rup.pyt | TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCTCAGCAA | 60 |
| rup.rup | TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCAGCAA | 60 |
| nem.cau | TACCATGAGGACAGATATCATTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCAGCAA | 60 |
| bud.tax.tax | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| pan.hod | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAAATTACCAACCTCTCTCTCAGCAA | 60 |
| ovi.amm | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCTCAGCAA | 60 |
| ovi.vig | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCTCAGCAA | 60 |
| cap.cri | TACCATGAGGACAAATATCATTCTGAGGGGGCTACAGTCATTACTAACCCTCTCTCTCAGCAA | 60 |
| ovi.mos | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| ore.ame | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| cep.dor | TCCCATGAGGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| cep.max | TCCCATGAGGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| bis.bon | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| bos.gru | TACCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |
| bos.tra | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA | 60 |
| bub.min | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| buba.bub | TGCCATGAGGACAAATATCATTCTGAGGGGGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| tra.ang | TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| tra.eur | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| kob.ell | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| kob.meg | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCCTAATCTCTCTCTCAGCAA | 60 |
| red.aru | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAATCTCTCTCTCAGCAA | 60 |
| red.ful | TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| neo.mos | TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| pel.cap | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| gas.dam | TACCATGAGGACAAATATCCTTCTGAGGGGGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| our.our | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| ant.cer | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| sal.tat | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCACCTCTCTCTCAGCAA | 60 |
| mad.kir | TGCCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| rap.mel | TACCATGGGGACAAATATCCTTCTGAGGAGCAACAGTCATCCTAATCTCTCTCTCAGCAA | 60 |
| gas.gas | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| ant.ame | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| hyd.lne | TGCCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCCTAACCCTCTCTCTCAGCAA | 60 |
| mun.ala | TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCCTAACCCTCTCTCTCAGCAA | 60 |
| alc.ala | TACCATGAGGACAGATATCCTTCTGAGGGGGCAACAGTTATTACCAATCTCTCTCTCAGCAA | 60 |
| cec.ela.kun | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCTCAGCAA | 60 |

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|--------------|---|----|
| cer.ela.xan | TACCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTTCTCTCAGCAA | 60 |
| cer.ela.can | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA | 60 |
| cer.nip.cent | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA | 60 |
| cer.nip.yes | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA | 60 |
| cer.nip.ker | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA | 60 |
| cer.nip.pul | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA | 60 |
| cer.nip.nip | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA | 60 |
| cer.ela.sco | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA | 60 |
| cer.dam | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA | 60 |
| ran.tar | TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACAAACCTCCTCTCAGCAA | 60 |
| mos.fus | TACCTTGAGGACAAATATCTTTCTGAGGAGCGACAGTTATTACCAATCTTCTCTCAGCAA | 60 |
| mos.leu | TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA | 60 |
| mos.chr | TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA | 60 |
| mos.ber | TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA | 60 |
| mos.mos | TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACTAACCTTCTCTCAGCAA | 60 |
| tra.jav | TACCCTGAGGACAGATATCTTTCTGAGGAGCCACAGTCATCACCAACCTCTTATCAGCTA | 60 |
| trag.nap | TACCCTGAGGGCAAATATCTTTTGGAGGAGCTACAGTCATCACTAACCTTCTTTTCAGCAA | 60 |
| bala.acu | TACCCTGAGGACAAATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| bala.bon | TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| bala.bor | TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| bala.edi | TACCCTGAGGACAAATATCATTTTGGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| esch.rob | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA | 60 |
| bala.mus | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| mega.nov | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTTCTATCAGCAA | 60 |
| bala.phy | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCCTATCAGCAA | 60 |
| cap.mar | TGCCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| ceph.com | TACCCTGSGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| ceph.eut | TACCCTGSGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| lage.obl | TACCCTGAGGACAGATATCATTCTGAGGCGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| ceph.heu | TACCCTGAGGACAAATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| ceph.hec | TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| lage.aus | TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| lage.cru | TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| lage.obs | TACCCTGAGGACAGATATCATTTTGGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA | 60 |
| lisso.bor | TACCCTGAGGGCAGATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| lisso.per | TACCCTGAGGACAGATATCATTTTGGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
| glo.mac | TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| glo.mel | TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| fere.att | TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| pepo.ele | TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| gram.gri | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| pse.cra | TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTTCTATCAGCAA | 60 |
| lage.acu | TACCATGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAATCTCCTATCAGCAA | 60 |
| ordi.bre | TACCCTGAGGACAGATATCTTTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA | 60 |
| orca.bre | TACCCTGAGGACAGATATCCTTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA | 60 |
| del.cap | TGCCCTGSGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| del.tro | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| del.del | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| sten.cly | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| sten.coe | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| tur.adu | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| sten.fro | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA | 60 |
| saus.chi | TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA | 60 |
| sten.lon | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA | 60 |
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| lage.alb | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA | 60 |
| sten.bre | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAACCTCCTGTAGCAA | 60 |
| sota.flu | TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA | 60 |

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| pero.pot | TCCCATGAGGACAAATATCATTCTGAGGCTGCCACAGTAATCACAAACCTCCTATCAGCAA | 60 |
| gala.mat | TCCCATGAGGACAAATATCATTCTGAGGCGCTACCGTAATCACAAATCTCCTCTCCGCAA | 60 |
| gala.moh | TTCCGTGAGGACAAATATCATTCTGAGGCGCTACCGTAATCACTAACCTCCTCTCAGCAA | 60 |
| oto.gar | TCCCATGAGGACAAATGTCTATTCTGAGGCGCAACCGTAATTACAAATCTCCTCTCAGCAA | 60 |
| lor.tar | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACCAACCTACTATCAGCAA | 60 |
| nyc.cou | TCCCATGAGGACAAATATCATTCTGAGGCTGCCACCGTCATCACTAACCTACTATCAGCAA | 60 |
| mus | TTCCATGAGGACAAATATCATTCTGAGGCTGCCACAGTTATTACAAACCTCCTATCAGCAA | 60 |
| gorr | TCCCATGAGGACAAATATCCTTCTGAGGAGCCACAGTAATCACAAACCTTGTATCCGCAA | 60 |
| homo | TCCCGTGAGGACAAATATCATTCTGAGGCGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| dug.dug | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ele.max | TTCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| afr.con | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| pavo.mut | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| tra.bly | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| tra.sat | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| tra.cob | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| tra.tem | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| arg.arg | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
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| fra.fra | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ith.cru | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ant.par | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ant.vir | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| gru.ant.ant | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
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| gru.can.pra | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
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| gru.mon | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| gru.nig | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| gru.jap | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| cic.boy | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| rhe.ame | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ant.alb | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| fal.fam | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
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| ayt.ame | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| smi.sha | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| vid.cha | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| chry.pic | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| emy.orb.kur | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| che.mud | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| eum.egr | TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACAAACCTTACTATCCGCAA | 60 |
| ... | ... | ... |
| sep.mel | TCCCATATATTGGCACAAACCTTACTAGTAATTAATTTGAGGAGGATTCTCTTACTAGCAAAAG | 120 |
| ore.ore | TTCCATATATTGGCACAAACCTTACTAGTAATTAATTTGAGGAGGATTCTCTTACTAGCAAAAG | 120 |
| add.nas | TCCCATATATTGGCACAAACCTTACTAGTAATTAATTTGAGGAGGATTCTCTTACTAGCAAAAG | 120 |

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| ory.dam | TCCCATACATCGGCACAAATCTAGTCGAATGAATTTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| hip.equ | TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| alc.bus | TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| sig.lic | TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| bea.hun | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| dam.lun | TTCCATACATCGGCACAAATCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| con.tau | TCCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| amm.ler | TCCCATACATTGGGCACAGACCTGGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| pse.nay | TCCCATATATTGGGCACAAATCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cap.ibe | TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| hem.jem | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cap.fal | TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| rup.pyr | TCCCATACATTGGGCATAGACTTAGTCGAGTGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| rup.rup | TCCCGTATATTGGGCACAGACTTAGTCGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| nem.cau | TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| bud.tax.tax | TCCCATACATTGGGCACAAACCTAGTTGAGTGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| pan.hod | TCCCATACATTGGGCACAGACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| ovi.amm | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| ovi.vig | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cap.cri | TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| ovi.mos | TCCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| ore.ame | TTCCATACATCGGTACAGACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cep.dor | TCCCATACATTGGGTACAAACTTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cep.max | TCCCATATATCGGCACAAACTTAGTTGAGTGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| bis.bon | TCCCATACATCGGCACAAATCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| bos.gru | TTCCATACATCGGCACAAATTTAGTCGAATGGATTTGAGGTGGGTTCTCAGTAGACAAAAG | 120 |
| bos.tra | TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| bub.min | TCCCATACATTGGGCACAAACCTAGTTGAGTGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| buba.bub | TCCCATACATTGGGTACAACTCTGGTTGAATGAATTTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| tra.ang | TCCCATATATTGGGCACCAACCTAGTTGAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| tra.eur | TCCCTTATATTGGGCACCAGCCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| kob.ell | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAGG | 120 |
| kob.meg | TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| red.aru | TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTCGATAAAG | 120 |
| red.ful | TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGATTCTCAGTCGATAAAG | 120 |
| neo.mos | TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| pel.cap | TCCCATACATTGGGTACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| gas.dam | TCCCATACATCGGCACAGACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGATAAGG | 120 |
| our.our | TTCCATACATTGGGTACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| ant.cer | TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| sai.tac | TCCCATATATCGGCACAGACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| mad.kir | TCCCATATATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| rap.mel | TTCCCTACATTGGGCACAAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTTGATAAAG | 120 |
| gas.gas | TCCCATACATCGGCACAAACCTAGTAGAATGAATCTGAGGGGGATTCTCGGTAGATAAAG | 120 |
| ant.ame | TCCCATACATTGGGTACTAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| hyd.ine | TTCCATACCTCGGTACAAATCTAGTCGAATGAATCTGAGGGGGATTCTCAGTTGATAAAG | 120 |
| mun.mun | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTTGATAAAG | 120 |
| alc.alc | TTCCATACATTGGGTACTAATCTAGTTGAATGAATTTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cer.ela.kan | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.ela.kan | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.ela.gin | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.nip.cen | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.nip.yes | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.nip.ker | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.nip.pul | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.nip.nip | TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGATAAAG | 120 |
| cer.ela.gin | TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |
| cer.dam | TTCCATACATTGGGTACAAACTAGTTGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG | 120 |

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| ran.car | TTCCATATATTGGTACAAATCTAGTCCAATGAATTTGAGGAGGATTTTCTGTAGATAAAG | 120 |
| mos.fus | TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCACTAGACAAAAG | 120 |
| mos.leu | TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCACTAGACAAAAG | 120 |
| mos.chr | TTCCATACATTGGTACTAATCTGGTTGAATGAATTTGAGGAGGCTTCTCACTAGACAAAAG | 120 |
| mos.ber | TTCCCTTACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCACTAGACAAAAG | 120 |
| mos.mos | TTCCCTTACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCACTAGACAAAAG | 120 |
| tra.jav | TCCCATAACATTGGGACAGACTTGGTCCAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| trag.nap | TCCCCTATATTGGGACCCGAAGTAGTTGAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| bala.acu | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| bala.bon | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| bala.bor | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| bala.edi | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTAGACAAAAG | 120 |
| esch.rob | TCCCATAACATTGGGACTACCTTAGTCCAATGGGTCTGAGGCGGGTTCTCACTAGATAAAG | 120 |
| bala.mus | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTGGATAAAG | 120 |
| mega.nov | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCCGTAGACAAAAG | 120 |
| bala.phy | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCACTAGATAAAG | 120 |
| cap.mar | TCCCATAACATTGGTACTACCTTAGTCCAATGAATCTGAGGCGGGTTCTCCGTAGACAAAAG | 120 |
| ceph.com | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| ceph.eut | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lage.obl | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| ceph.heu | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGAGGATTTTCCGTAGACAAAAG | 120 |
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| lage.aus | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lage.cru | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lage.obs | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lisso.bor | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lisso.per | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| glo.mae | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| glo.mel | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| fere.att | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| pepo.ele | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| gram.gri | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| pse.cra | TCCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| lage.acu | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| orci.bre | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| orca.bre | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| del.cap | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| del.tro | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
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| tur.adu | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| sten.fro | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| saus.chi | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| sten.lon | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| turs.tru | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| lage.alb | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| sten.bre | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| sota.flu | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAAG | 120 |
| del.leu | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCTGTAGATAAAG | 120 |
| mono.mon | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGATAAAG | 120 |
| plat.gan | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGATAAAG | 120 |
| plat.min | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| kogi.bre | TCCCCTATATTGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| kogi.slm | TCCCCTACATCGGCACTACCTTAGTCCAATGAATCTGAGGCGGATTTCTCCGTAGATAAAG | 120 |
| phys.gat | TCCCCTATATTGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTCTCCGTAGATAAAG | 120 |
| lipo.vak | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |
| phoc.slm | TCCCCTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTTCTCCGTAGACAAAAG | 120 |

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| bera.bai | TTCCCTTATATCGGCCACTACTCTTGTGCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG | 120 |
| ziph.car | TCCCTTATATCGGCCACTACTCTAGTTCGAATGAATCTGAGGTGGCTTTTTCAGTAGATAAAAG | 120 |
| meso.eur | TCCCTTATATTTGGCACTACTCTAGTTCGAATGAATCTGAGGTGGCTTTTCCGTAGATAAAAG | 120 |
| meso.bid | TTCCCTACATCGGCCACTACCCTAGTTGAATGAATCTGAGGTGGCTTTTCCGTAGACAAAAG | 120 |
| meso.den | TTCCCTTATATTTGGCAACCACCCTAGTTCGAGTGAATCTGAGGTGGCTTTTCCGTAGACAAAAG | 120 |
| hype.amp | TTCCCTTATATCGGCCACTACCCTAGTTGAATGAATCTGAGGTGGCTTCTCCGTAGACAAAAG | 120 |
| meso.per | TCCCTTATATTTGGCAACCACCCTAGTTGAATGAATTTTGAGGTGGCTTCTCCGTAGATAAAAG | 120 |
| pont.bla | TCCCTTACATCGGGAACCTACCCTTGTAGAAATGGATCTGAGGTGGCTTCTCTGTAGACAAAAG | 120 |
| hex.lib | TCCCTTACATTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGATAAAAG | 120 |
| hipp.amp | TCCCTTATATTTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCCGTAGACAAAAG | 120 |
| dic.sum | TCCCTACATCGGCCACCAGACCTTGTAGAAATGAATCTGAGGGGGATTCTCCGTAGACAAAAG | 120 |
| rhin.son | TCCCTTATATCGGTACCAACCTTGTAGAGTGAATCTGAGGAGGATTCTCAGTCGACAAAAG | 120 |
| cera | TCCCTTACATCGGCCACCAACCTCGTAGAATGAATCTGAGGAGGATTCTCCGTGACAAAAG | 120 |
| equu | TCCCTTACATCGGTACTACGCTCGTAGAATGAATCTGAGGAGGATTCTCAGTAGACAAAAG | 120 |
| baby.bab | TTCCCTTATATCGGAACCGGACCTCGTAGAATGGATCTGAGGAGGCTTCTCCGTGACAAAAG | 120 |
| phac.afr | TCCCTTACATTGGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTCCGTGACAAAAG | 120 |
| sus.bar | TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCCGTGACAAAAG | 120 |
| lus.scr.ewb3 | TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCCGTGACAAAAG | 120 |
| lama.gla | TTCCATATGTTGGGACAGACCTAGTTCGAATGAATTTGAGGAGGATTCTCCGTAGACAAAAG | 120 |
| lama.gua | TTCCATATGTTGGGACAGACCTAGTTCGAATGAATTTGAGGGGGGTTCTCCGTAGATAAAAG | 120 |
| vic.vic | TTCCATACGTTGGTACAGACCTAGTTCGAGTGGATTGAGGAGGATTCTCCGTAGATAAAAG | 120 |
| cam.bac | TTCCCTTATATCGGGACAGACCTAGTAGAATGAATTTGAGGTGGCTTCTCCGTAGACAAAAG | 120 |
| arc.for | TCCCTTACATTGGGACCAACCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGATAAAAG | 120 |
| arc.gaz | TCCCTTACATCGGAACCTAACCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGATAAAAG | 120 |
| eum.jub | TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTTCAGTCGACAAAAG | 120 |
| sal.cal | TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTTCAGTCGACAAAAG | 120 |
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| pho.fasciata | TTCCCTTATATCGGAACCGGACCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGATAAAAG | 120 |
| pho.gro | TCCCTTACATCGGAACCGGATCTAGTAGAATGAATCTGAGGAGGTTCTCAGTTGATAAAAG | 120 |
| pho.vit | TCCCTTATGTTCGGAACCGGACCTTGTAGAATGAATCTGAGGAGGTTTTCAGTAGATAAAAG | 120 |
| cys.cri | TCCCTTACATCGGGAGCGGATCTAGTAGAATGAATCTGAGGGGGATTTCAGTCGATAAAAG | 120 |
| hyd.lep | TTCCCTTACATCGGAACCGGACCTAGTAGAATGAATTTGAGGCGGATTTCAGTCGACAAAAG | 120 |
| lep.wed | TTCCCTTACATCGGAACCTGACTTAGTAGAATGAATCTGAGGCGGATTTCAGTTGACAAAAG | 120 |
| mir.leo | TCCCTTATGTTCGGAGACGACCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGACAAAAG | 120 |
| eri.bar | TCCCTTACATCGGGAGCTGATCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGACAAAAG | 120 |
| mon.sch | TCCCTTACATCGGAACCGGATCTAGTAGAATGAATCTGAGGAGGATTTCAGTTGACAAAAG | 120 |
| hela.mal | TCCCTTATATTTGGGAACCGGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAAG | 120 |
| sel.thi | TCCCTTATATTTGGGAACAGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAAG | 120 |
| ail.ful | TTCCCTATATTTGGGAACCTAACCTTGTAGAGTGAATCTGAGGAGGTTTCTCAGTCGACAAAAG | 120 |
| fel | TTCCATACATCGGGAGCTGAACCTAGTAGAATGAATCTGAGGGGGCTTCTCAGTAGACAAAAG | 120 |
| can | TCCCTTATATCGGAACCTGACTTAGTAGAATGGATCTGAGGCGGCTTCTCAGTCGACAAAAG | 120 |
| tal | TTCCCTTACATCGGTACAGACTTAGTAGAATGAATTTGAGGTGGCTTCTCAGTCGACAAAAG | 120 |
| gla.sab | TTCCCTTATATTTGGGACAAACCTTGTAGAATGAATCTGAGGAGGCTTCTCTGTGACAAAAG | 120 |
| gla.vol | TTCCCTTATATTTGGTACAAACCTTGTAGAATGAATCTGAGGGGGCTTCTCTGTGATAAAAG | 120 |
| hyl.pha | TCCCTTACATTGGGAACAGTCTCTGTGGAATGAATTTGAGGGGGATTTCCTGTAGATAAGG | 120 |
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| bel.pea | TCCCTTATATTTGGGAACAGTCTCTGTGGAATGAATTTGAGGGGGATTTCCTGTAGATAAGG | 120 |
| pte.mom | TCCCTTATATCGGGACCAACCTTGTGGAATGGATCTGAGGTGGCTTCTCAGTTGATAAAAG | 120 |
| gala.demi | TCCCTATATATACGGGCTACTCTAGTAGAATGAATCTGAGGGGGCTTTTCCGTAGACAAAAG | 120 |
| pero.pot | TCCCTATATATAGGTAGAACCCCTGTAGAATGAATTTGAGGGGGATTTCCTCAGTAGACAAAAG | 120 |
| gala.mat | TTCCCTTACATCGGTACGGGCTAGTAGAATGAATCTGAGGGGGATTTCCTCAGTAGACAAAAG | 120 |
| gala.moh | TTCCCTTATATAGGAACCTAGTAGAATGAATCTGAGGGGGATTTCCTCAGTAGACAAAAG | 120 |
| oto.gar | TTCCCTTACATCGGAACCTAACCTAGTTGAATGAATCTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |
| lps.bar | TTCCCTTATATTTGGGACAAACCTAGTTGAATGAATTTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |
| lys.cou | TCCCTTACATCGGAACAGACCTAGTTGAATGAATTTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |
| mus | TCCCTTATATTTGGGAACAAACCTAGTTGAATGAATTTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |
| gact | TCCCTTACATCGGAACAGACCTAGTTGAATGAATTTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |
| homo | TCCCTTACATTGGGACAGACCTAGTTGAATGAATTTGAGGGGGATTTCCTCAGTAGATAAAAG | 120 |

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| dug.dug | TCCCCTACATCGGGACCAACCTAGTCGAATGAGTTTGAGGGGGGATTCTCAGTAGACAACG | 120 |
| ele.max | TTCCCCTACATCGGGACCAACCTAGTAGAATGAAATTTGAGGAGGGCTTTTCGGTAGATAAAG | 120 |
| afr.con | TCCCCTATATTGGTCAAACCTAGTAGAATGGGCTTGAGGAGGATTCTCAGTTGACAACC | 120 |
| pavo.mut | TCCCCTTATATTGGACAAACCTAGTAGAATGAGCCTTGAGGGGGATTCTCAGTCGACAACC | 120 |
| tra.bly | TCCCATACATTTGGCCAAACCTTAGTAGAATGAGCCTTGAGGAGGGCTTTTCAGTTGACAATC | 120 |
| tra.sat | TCCCATACATTTGGTCAAACCTAGTAGAATGAGCCTTGAGGCGGGCTTTTCAGTTGACAATC | 120 |
| tra.cob | TCCCATACATTTGGCCAAACCTTAGTAGAATGGGGCTTGAGGGGGCTTTTCAGTTGACAATC | 120 |
| tra.tem | TCCCATACATTTGGCCAAACCTAGTAGAATGAGCCTTGAGGGGGCTTTTCAGTTGACAATC | 120 |
| arg.arg | TCCCCTATATTGGACAAACCTAGTAGAGTGAGCCTTGAGGAGGATTCTCAGTCGACAACC | 120 |
| cat.wal | TCCCCTACATCGGACAGACCCTAGTAGAATGAGCCTTGAGGAGGATTCTCAGTTGACAATC | 120 |
| cro.cro | TCCCCTACATTTGGACAAACCTAGTCGAGTGAGCTTGAGGGGGATTCTCAGTTGACAACC | 120 |
| sym.ree | TCCCCTACATCGGACAAACCTAGTAGAGTGAGCTTGAGGGGGATTCTCAGTAGACAACC | 120 |
| bam.tho | TTCCCCTACATCGGACAAACCTAGTAGAATGAGCCTTGAGGGGGATTCTCAGTAGACAACC | 120 |
| fra.fra | TTCCCCTACATTTGGCCAAACCTTAGTAGAGTGAGCCTTGAGGGGGATTCTCAGTAGACAACC | 120 |
| ich.cru | TTCCCCTACATCGGGCCAAACCTCTGTTAGAATGAGCTTGAGGAGGATTCTCAGTAGACAACC | 120 |
| ant.par | TCCCATATATCGGGCCAAACCTTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| ant.vir | TCCCATACATCGGGCCAAACCTTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGATAATC | 120 |
| gru.ant.ant | TCCCCTACATCGGGCCAAACCTTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
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| gru.ant.sha | TCCCCTACGGGGCCAAACCTTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.leu | TCCCCTACATCGGGCCAAACCTTTGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.can.pra | TCCCATACATCGGGCCAAACCTTCGTAGAATGGGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.can.row | TCCCATACATCGGGCCAAACCTTCGTAGAATGGGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.can.tab | TCCCATACATCGGGCCAAACCTTCGTAGAATGGGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.can.can | TCCCATACATCGGGCCAAACCTTCGTAGAATGGGCTTGAGGGGGCTTTCTCAGTAGACAATC | 120 |
| gru.ame | TCCCATACATCGGGCCAAACCTTCGTAGAATGAGCTTGAGGGGGCTTTCTCTGTAGACAACC | 120 |
| gru.gru | TCCCATACATCGGGCCAAACCTTCGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAACC | 120 |
| gru.mon | TCCCATACATCGGGCCAAACCTTCGTAGAATGAGCTTGAGGAGGCTTTCTCAGTAGACAACC | 120 |
| gru.nig | TCCCATACATCGGGCCAAACCTTCGTAGAATGAGCTTGAGGAGGCTTTCTCAGTAGACAACC | 120 |
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| cic.boi | TCCCCTACATCGGGCCAAACCTTCGTAGAATGGGCTTGAGGGGGCTTTCTCGGTGATAACC | 120 |
| rhe.ame | TCCCCTACATCGGACAAACCTTTGGTAGAATGAGCTTGAGGGGGCTTTCTCAGTAGACAACC | 120 |
| ant.alb | TCCCATACATCGGGCCAAACCTTAGTAGAATGGGCTTGAGGGGGATTCTCTGTTGACAACC | 120 |
| fal.fam | TCCCATACATCGGTCAAACCTAGTCGAGTGAGCTTGAGGAGGATTCTCAGTAGACAATC | 120 |
| fal.ver | TCCCATACATCGGGCCAAACCTAGTCGAATGGGCTTGAGGAGGATTCTCAGTAGATAACC | 120 |
| fal.per | TCCCATACATCGGGCCAAACCTAGTCGAATGAGCTTGAGGGGGATTCTCAGTAGACAACC | 120 |
| fal.spa | TCCCATATATCGGGCCAAACCTAGTCGAATGGGCTTGAGGAGGATTCTCAGTAGACAACC | 120 |
| ayc.ame | TCCCATACATCGGGCCAAACCTTTGTAGAATGGGCTTGAGGAGGATTCTCTGTTGACAACC | 120 |
| smi.sha | TTCCATACATCGGACAAACCTAGTAGAATGAGCTTGAGGAGGATTCTCAGTAGACAACC | 120 |
| vid.cha | TTCCATACATTTGGCCAAACCTAGTAGAATGAGCCTTGAGGAGGATTCTCAGTAGACAACC | 120 |
| chry.pic | TCCCATTTCATTGGTAACACATTAGTAGAATGAAATCTGAGGTGGAATCTCAGTAGACAACC | 120 |
| emy.orb.kur | TCCCATACATTTGGCAATACACTAGTGCAATGAAATCTGAGGGGGATTCTCAGTAGATAACC | 120 |
| che.mud | TCCCATACATCGGGCAACACACTAGTAGAATGAAATCTGAGGGGGATTCTCAGTAGACAATC | 120 |
| eum.egr | TTCCATACATTTGGCCAAACCTAGTAGAATGAAATTTGAGGGGGCTTTCTCAGTAGACAACC | 120 |
| * * * * * | | |
| sep.mel | CAACCCCTNACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| ore.ore | CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| add.nas | CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| ory.dam | CAACCCCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| hip.equ | CAACCCCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| als.bus | CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
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| bea.hun | CAACCCCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| dum.lun | CAACCCCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| con.fur | CAACCCCTTACCCGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| amm.les | CTACTCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |
| pon.nay | CTACTCTCACCCTGATTCTTTGGCTTTCAGCTTCATCTTTGATTTCATTTCGCGGACTAG | 130 |

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|-------------|-------------|----------|--------|--------|----------|-------|---------|---------|--------|-----|
| cap.ibe | CCACTCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| hem.jem | CTACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cap.fal | CCACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| rup.pyr | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| rup.rup | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| nem.cau | CTACTCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| bud.tak.tak | CATCCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| pan.hod | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| ovi.amm | CCACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| ovi.vig | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cap.cri | CCACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| ovi.mos | CCACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| ore.ame | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cep.dor | CAACTCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
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| bos.tra | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| bub.min | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| buba.bub | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
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| tra.eur | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| kob.ell | CAACCCTTACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
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| red.aru | CAACCCTTACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| red.ful | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| neo.mos | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| pel.cap | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| gas.dam | CAACTCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| our.our | CAACTCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| ant.cer | CAACCCTTACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
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| hyd.ine | CTACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| mun.mun | CAACCCTCACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| alc.alc | CAACTCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cer.ela.kan | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cer.ela.xan | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cer.ela.can | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC | CCATT | CCATCAT | ATTACAG | CCCTCG | 130 |
| cer.nip.cen | CAACCCTAACC | CGATTCTT | CGCCTT | CCACTT | CGCTCC</ | | | | | |

[illegible]

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|--------------|---|-----|
| hipp.amp | CCACCCTTACACGATTCTTTGGCTTCCACTTTATTCTTCCATTTCOTTATCACAGCACTAG | 120 |
| dic.sum | CCACCCTCACCCGGTTCTTTGGCTTTCACATTCCTCCCTTCATCATCCTAGCCCTAG | 130 |
| rhin.son | CTACCCTTACCCGATTCTTTGGCTTTCACATTCCTCCCTTTATTATCCTAGCCTAG | 130 |
| cera | CCACACTTACACGATTCTTTGGCTTTCACATTCCTCCCTTTATTATCATAGCCCTAG | 130 |
| equu | CCACCCTTACCCGATTCTTTGGCTTTCACATTCCTACCTTTATCATCACAGCCCTGG | 130 |
| baby.bab | CAACCCTCACACGATTCTTTGGCTTTCACATTCCTACCTTCATCATCACCCCTCTCG | 130 |
| phac.afr | CAACTCTCACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| sus.bar | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| sus.ser.ewb3 | CAACCCTCACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| lama.gla | CCACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| vic.vic | CCACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| cam.bac | CCACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| arc.for | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| arc.gaz | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| eum.jub | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| zal.cal | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| odo.ros | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| pho.fasciata | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| pho.gro | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| pho.vit | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| cys.cri | CAACTCTAACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| hyd.lep | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| lep.wed | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| mir.leo | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| eri.bar | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| mon.sch | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| hela.mal | CGACTCTAACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| sel.chi | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| can | CAACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| tal | CGACACTCACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| gala.mat | CCACCCTTACTCGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| gala.moh | CTACTCTTACCCGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| oto.gar | CAACCCTCACCCGGTTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| nyo.cou | CCACACTCACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
| mus | CCACCTTGACCCGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| homo | CCACCCTTACACGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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| tea.bly | CAACCCTTACCCGATTCTTTGGCTTTCACATTCCTACCTTTATCATCGCTGCCCTAG | 130 |
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 sym.ree CAACCCCTCACCCGATTCTTCCGCCCTTCACTTTCTCCTACCCCTTCCTAATTCACAGGAATCA 130
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 ith.cru CAACCCCTCACCCGATTCTTCCGCCCTACACTTCCTTCTCCGCCCTTCGCAATTCGAGGAATTA 130
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 ant.vir CCACATTAACTCGATTCTTTCACCTTTACACTTCCTCCTTCCTTCATTTCATAATTATGGGCCCTCA 130
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aep.mel CCATAGTCCACCTACTCTTTCTCCAGAAACAGGATTTAAACAACCCCTACAGGAATCTTAT 240
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lisso.bor CAGCTGTTACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240
lisso.per CAGCTGTTACCTACTGTTCTACACGAGACAGGATCCAATAACCCCATAGGAATCCCAT 240
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sten.lon CAGCCGTTACCTACTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240
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sten.bre CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAATCCACAGGAATCCCAT 240
sota.flu TAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240
del.leu TGGCCGTCACCTATTATTCTACACGAAACAGGATCCAACAACCCACAGGAATCCCAT 240
mono.mon CAATTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCACAGGAATCCCAT 240
plat.gan CAGTTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCACAGGAATCCCAT 240
plat.min CAATGGTCCACCTCTATTCTTCTCCAGAAACAGGATCCAACAACCCCATAGGAATCCCAT 240
kogi.bre CAATAATCCACCTCTATTCTTCTCCAGAAACAGGATCCAACAACCCCTAGGAATTCCTT 240
kogi.sim CAATAGTACATCTCTATTCTTCTCCATGAAACAGGATCCAACAACCCACAGGAATTCCTT 240
phys.cac CAACCGTCCACTTACTATTCTTCTCCATGAAACAGGATCCAACAACCCATAGGAATTCCTT 240
lipo.vex TAATCGTCCATCTACTATTCTTCTCCATGAAACAGGCTCCAACAATCCACAGGAATCCCAT 240
phoc.sin CAGCCGTCACCTACTATTCTTCTCCAGAAACAGGATCCAACAACCCACAGGAATCCCAT 240
bera.bai CAGCCGTCACCTACTATTCTTCTCCAGAAACAGGATCTAATAACCCACAGGAATCCCAT 240
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hype.amp TTATAGTCCACCTGCTATTCTTCTACACGAAACAGGATCCAACAACCCACAGGAATTCCTT 240
meso.per CCGCCGTCACCTACTGTTTCTCCAGAAACAGGCTCCAACAACCCACAGGAATTCCTT 240
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hex.lib CAATTAGCCACCTGCTATTCTTCTACACGAAACAGGATCCAATAACCCATCAGGAATTCCTT 240
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dic.sum CAATCAGCCACCTACTATTCTTCTACGAAACAGGATCCAATAACCCATCAGGAATTCCTT 240
rhin.son TAATCGTCCATCTACTATTCTTCTCCAGAAACAGGATCCAACAACCCCTACTGGAATTCCTT 240
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equu GAACCGTACATCTCTTTCTTCTACGAAACAGGATCTAATAACCCCTACTGGAATTCCTT 240
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| | | |
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| eum.jub | TAATAGTACACCTATTATTCTTACACGAAACAGGATCCAACAATCCAATCAGGAATCTCCT | 240 |
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| odo.ros | CAGCAGTACACCTACTATTCTTACACGAAACAGGATCCAACAACCCCTCCGGAATCGTAT | 240 |
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| pho.vit | CAGCAGTCCACCTACTATTCTTACACGAAACAGGATCCAACAACCCCTCCGGAATCATAT | 240 |
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| mir.leo | CAGCAGTACATCTACTATTCTTACACGAAACAGGATCCAACAACCCCTCTGGAATCCCAT | 240 |
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| sel.thi | CAGCAGTTACCTATTGTTCTTACACGAAACAGGATCCAACAACCCCTCTGGAATCCCAT | 240 |
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| fel | CAGGAGTACACCTCTTATTCTTCTTACGAAACAGGATCTAACAACCCCTCAGGAATTACAT | 240 |
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| gorr | CCCCTCTGACAAAAATCCCATTTCCACCCGTACTACACAAATTTAAAGACATCCTAGGCCTAT | 300 |
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| cic.boy | CAAACCTGCGACAAAATCCCATTCACCCCTACTTCTCCCTCAAAGATATCCTAGGCTTCA | 300 |
| rhe.ame | CTCACTCTGACAAAATCCCATTCACCCCTACTTCTCCCTCAAAGATATCCTAGGACTAG | 300 |
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| fal.per | CAAATTGCGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGATATCCTAGGATTCA | 300 |
| fal.spa | CAAACCTGTGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGACCTCCTAGGTTTCA | 300 |
| ayt.ame | CAGACTGCGACAAAATCCCATTCACCCCTACTTCTCCTTCAAAGACATCCTAGGATTCA | 300 |
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| lipo.vex | ATTTCCCTCTTCGCATACGCAATTCTACGATCAATTCCCAATAAACTAGGAGG | 472 |
| phoc.sin | ATTTCCCTCTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG | 472 |
| bera.bai | ACTTCCTGTTTCGCATACGCAATCTTACGATCAGTCCCTAATAAACTAGGGGG | 472 |
| ziph.car | ACTTCCTATTTCGCATACGCAATCCTACGATCAATTCCCAATAAACTAGGAGG | 472 |
| meso.eur | ACTTCCTATTTCGCATATGCAATTCTACGATCAATTCCCAATAAACTAGGAGG | 472 |
| meso.bid | ATTTCCCTATTTCGCATACGCAATCTTACGATCAATTCCCTAATAAACTAGGAGG | 472 |
| meso.den | ATTTTCTATTTGCGATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG | 472 |
| hype.amp | ACTTCCTATTTGCGATACGCAATCCTACGTTCAATCCCTAATAAACTAGGAGG | 472 |
| meso.per | ATTTTCTATTTGCGATATGCAATTTTACGATCAGTTCTAATAAACTAGGAGG | 472 |
| pont.bla | ATTTCCCTATTTGCGTACGCCATCCTACGATCAATTCCCAATAAACTGGGAGG | 472 |
| hex.lib | ATTTCCCTGTTTCGCATACGCAATCTCCGATCAATCCCTAATAAACTGGGAGG | 472 |
| hipp.amp | ATTTCCCTGTTTCGCGTACGCGATTCTCCGATCAATCCCCAATAAACTAGGAGG | 472 |
| dic.sum | ACTTCCTATTTCGCTACGCAATCCTACGATCCATCCCCAATAAACTAGGCCG | 472 |
| rhin.son | ATTTCCCTATTTGCTTACGCAATCCTACGATCCATCCCCAATAAACTAGGCCG | 472 |
| cera | ACTTTCTATTTGCTTACGCAATCCTACGATCCATCCCTAATAAACTAGGCCG | 472 |
| equu | ATTTCCCTATTTGCTTACGCCATCCTACGCTCCATTCCCCAATAAACTAGGTGG | 472 |
| baby.bab | ACTTCCTATTTGCGTACGCCATCCTACGCTCAATCCCCAATAAACTAGGTGG | 472 |
| phac.afr | ACTTCCTATTTCGCGTACGCCATCCTACGTTCAATCCCTAATAAACTAGGTGG | 472 |
| sus.bar | ACTTCCTATTTCGCGTACGCTATTTCTACGTTCAATCCCTAATAAACTAGGTGG | 472 |
| sus.scr.ewb3 | ATTTCTTATTTCGCGTACGCTATTTCTACGTTCAATCCCTAATAAACTAGGTGG | 472 |
| lama.gla | ACTTCCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| lama.gua | ACTTCCTATTTGCGTATGCTATTTCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| vic.vic | ATTTCCCTATTTGCGTATGCTATTTCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| cam.bac | ATTTCCCTATTTCGCGTATGCTATTTCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| arc.for | ATTTTCTATTTCGCTTACGCCATTTTACGATCTATCCCCAATAAACTAGGTGG | 472 |
| arc.gaz | ATTTTCTATTTCGCGTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| eum.jub | ATTTCCCTATTTCGCGTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| zal.cal | ATTTCCCTATTTCGCGTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| odo.ros | ATTTCCCTATTTCGCGTATGCTATTTTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| pho.fasciata | ACTTTCTATTTGCGTACGCCATCCTACGATCAATCCCCAATAAACTAGGTGG | 472 |
| pho.gro | ACTTTTCTATTTGCGTACGCCATCCTACGATCAATCCCCAATAAACTAGGTGG | 472 |
| pho.vit | ACTTCCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| cys.cri | ACTTCCTATTTCGCGTATGCAATCCTACGATCTATCCCCAATAAACTAGGTGG | 472 |
| hyd.lep | ATTTCCCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| lep.wed | ATTTCCCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| mir.leo | ATTTCCCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| eri.bar | ATTTCCCTATTTCGCGTATGCAATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| mon.sch | ACTTCCTATTTCGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| hela.mal | ACTTTCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| sel.chi | ACTTTTCTATTTGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| ail.ful | ATTTCCCTATTTCGCGTATGCAATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| fel | ACTTCCTATTTCGCGTACGCCATCCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| can | ATTTTCTATTTCGCGTATGCTATTTCTACGATCCATCCCCAATAAACTAGGTGG | 472 |
| tal | ACTTCCTATTTGCGTATGCGATCCTACGATCAATTTCTAATAAACTAGGTGG | 472 |
| gla.sab | ACTTTCTATTTGCGTATGCGATCCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| gla.vol | ACTTTCTATTTGCGTATGCGATCCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| hyl.pha | ACTTTCTATTTGCGTATGCGATCCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| pet.set | ACTTTCTATTTGCGTATGCGATCCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| bel.pea | ACTTTCTAATTTTATTCGCAATCCTTCGATCCATCCCCAATAAACTAGGTGG | 472 |
| pte.mom | ATTTCCCTATTTCGCGTATGCTATTTCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| gala.demi | ATTTCCCTATTTGCGTACGCCATCCTACGATCTATTTCTAATAAACTAGGTGG | 472 |
| pero.poc | ACTTTCTATTTGCGTACGCCATCCTACGATCCATTTCTAATAAACTAGGTGG | 472 |
| gala.mat | ACTTCCTATTTGCGTATGCGATCCTTCGATCAATTTCTAATAAACTAGGTGG | 472 |
| gala.mon | ACTTCCTATTTGCGTATGCGATCCTTCGATCAATTTCTAATAAACTAGGTGG | 472 |
| oto.gar | ATTTCCCTATTTGCGTATGCTATTTCTACGATCCATTTCTAATAAACTAGGTGG | 472 |
| lor.car | ATTTCCCTATTTCGCGTACGCCATCCTACGATCAATTTCTAATAAACTAGGTGG | 472 |

| | | |
|-----------------|--|-----|
| nyc.cou | ATTTTCTATTTCGGCTACGCCATCCTTCGATCAATCCCCAACAACTAGGAGG | 472 |
| mus | ATTTTCTATTTCGCATACGCCATTCTACGCTCAATCCCCAATAAACTAGGAGG | 472 |
| gorr | ATTTTCTATTTCGGCTACGCCAATTCTCCGATCTGTCCCCAATAAACTAGGAGG | 472 |
| homo | ATTTTCTATTTCGGCTACACAATTCTCCGATCCGTCCTAACAACAACTAGGAGG | 472 |
| dug.dug | ACTTTTCTATTTCGGATACGCTATCCTCCGATCTATCCCTAATAAACTAGGCGG | 472 |
| ele.max | ACTTTCTTTTGTGCTTACGCCATTCTACGATCTGTACCAAAACAACTAGGAGG | 472 |
| afr.con | ATTTTCTATTTCGGCTATGCCATCCTTCGCTCAATCCCCAACAACTAGGAGG | 472 |
| pavo.mut | ACTTTCTTATTTCGGCTACGCCATCCTTCGTTCAATCCCCAACAACTAGGAGG | 472 |
| tra.bly | ACTTTCTTATTTCGGCTACGCCATCCTTCGTTCAATCCCCAACAACTAGGAGG | 472 |
| tra.sat | ACTTTCTTATTTCGGCTACGCCATCCTTCGTTCAATCCCCAACAACTAGGAGG | 472 |
| tra.cob | ATTTTCTGTTTCGCTTATGCCATCCTACGCTCAATCCCCAACAACTCGGAGG | 472 |
| tra.tem | ATTTTCTGTTTCGCTTATGCCATCCTACGCTCAATCCCCAACAACTCGGAGG | 472 |
| arg.arg | ACTTTCTTATTTCGGCTATGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| cat.wal | ACTTTCTTATTTCGGCTACGCTATCCTACGCTCAATCCCCAATAAACTCGGAGG | 472 |
| cro.cro | ACTTTCTTATTTCGGCTATGCCATCCTTCGCTCAATCCCCAATAAACTCGGAGG | 472 |
| sym.ree | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTGGGGGG | 472 |
| bam.tho | ACTTTCTTATTTCGGCTATGCCATCCTACGCTCAATCCCCAACAACTCGGAGG | 472 |
| fra.fra | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTCGGAGG | 472 |
| ith.cru | ACTTTCTTATTTCGGCTACGCTATCCTACGCTCAATCCCCAATAAACTTGGAGG | 472 |
| ant.par | ATTTTCTTATTTCGGCTATGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| ant.vir | ATTTTCTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.ant.ant | ACTTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.ant.gil | ACTTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.ant.sha | ACTTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.leu | ACTTTCTTATTTCGCATACGCCATCCGACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.can.pra | ACTTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| gru.can.row | ACTTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| gru.can.tab | ACTTTTTTATTTCGGCTACTCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| gru.can.can | ACTTTTTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| gru.ame | ACTTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.gru | ACTTTTTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.mon | ACTTTTCTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.nig | ACTTTCTTATTTCGCATACGCTATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| gru.jap | ACTTTCTTATTTCGCATACGCTATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| cic.boy | ACTTTCTTATTTCGCATACGCCATCCTACGTTCAATCCCCAACAACTAGGAGG | 472 |
| rhe.ame | ATTTTCTTATTTCGCATATGCCATCCTACGCTCAATCCCCAATAAACTAGGAGG | 472 |
| ant.alb | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| fal.fam | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| fal.ver | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| fal.per | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| fal.spa | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| ayt.ame | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCAATCCCCAACAACTAGGAGG | 472 |
| smi.sha | ATTTTTTATTTCGCATACGCTATCCTCCGATCAATCCCCAACAACTAGGAGG | 472 |
| vid.cha | ACTTTCTTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAACTAGGAGG | 472 |
| chry.pic | ACTTTCTTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAACTAGGAGG | 472 |
| emy.orb.kur | ACTTTCTTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAACTAGGAGG | 472 |
| che.mud | ACTTTCTTATTTCGGCTACGCCATCCTACGATCCATCCCCAACAACTAGGAGG | 472 |
| eum.egr. | ACTTTCTTATTTCGGCTACGCCATCCTACGCTCTATCCCCAACAACTAGGAGG | 472 |
| PRIMER 'mc5869' | CGATCAATCCCTAACAACCTAGGAGG | |

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=

(328 letters)

Database: Sequences from complete mitochondrial genomes
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

(bits) Value

| | | | |
|-----------------|--|-----|-------|
| ref NC_001700.1 | Felis catus mitochondrion, complete genome | 365 | e-101 |
| ref NC_001325.1 | Phoca vitulina mitochondrion, complete genome | 198 | 1e-51 |
| ref NC_002008.1 | Canis familiaris mitochondrion, complete g... | 190 | 4e-49 |
| ref NC_001602.1 | Halichoerus grypus mitochondrion, complete... | 180 | 3e-46 |
| ref NC_000884.1 | Cavia porcellus complete mitochondrial genome | 176 | 5e-45 |
| ref NC_001808.1 | Ceratotherium simum mitochondrion, complet... | 155 | 2e-41 |
| ref NC_001892.1 | Myoxus glis mitochondrion, complete genome | 153 | 8e-38 |
| ref NC_001788.1 | Equus asinus mitochondrion, complete genome | 151 | 3e-37 |
| ref NC_002073.1 | Orycteropus afer complete mitochondrial ge... | 149 | 1e-36 |
| ref NC_001821.1 | Dasyurus novemcinctus mitochondrion, comple... | 141 | 3e-34 |
| ref NC_001779.1 | R.unicornis complete mitochondrial genome | 135 | 2e-32 |
| ref NC_001569.1 | Mus musculus mitochondrion, complete genome | 133 | 7e-32 |
| ref NC_000889.1 | Hippopotamus amphibius mitochondrion, comp... | 125 | 2e-29 |
| ref NC_001640.1 | Equus caballus mitochondrion, complete genome | 125 | 2e-29 |
| ref NC_001794.1 | Macropus robustus mitochondrion, complete ... | 123 | 7e-29 |
| ref NC_000845.1 | Sus scrofa mitochondrion, complete genome | 121 | 3e-28 |
| ref NC_001665.1 | Rattus norvegicus mitochondrial genome | 121 | 3e-28 |
| ref NC_001567.1 | Bos taurus mitochondrion, complete genome | 121 | 3e-28 |
| ref NC_001643.1 | Pan troglodytes mitochondrion, complete ge... | 117 | 4e-27 |
| ref NC_001941.1 | Ovis aries mitochondrion, complete genome | 109 | 1e-24 |
| ref NC_002391.1 | Talpa europaea mitochondrion, complete genome | 103 | 7e-23 |
| ref NC_001913.1 | Oryctolagus cuniculus mitochondrion, compl... | 103 | 7e-23 |
| ref NC_001644.1 | Pan paniscus mitochondrion, complete genome | 101 | 3e-22 |
| ref NC_001807.2 | Human mitochondrion, complete genome | 99 | 4e-21 |
| ref NC_001601.1 | Balaenoptera musculus mitochondrion, compl... | 98 | 4e-21 |
| ref NC_002009.1 | Artibeus jamaicensis mitochondrion, comple... | 96 | 2e-20 |
| ref NC_001645.1 | Gorilla gorilla mitochondrion, complete ge... | 92 | 2e-19 |
| ref NC_001321.1 | Balaenoptera physalus mitochondrion, compl... | 90 | 1e-18 |
| ref NC_001610.1 | Didelphis virginiana mitochondrion, comple... | 80 | 9e-16 |
| ref NC_002082.1 | Hylobates lar mitochondrion, complete genome | 70 | 9e-13 |
| ref NC_001727.1 | Crossostoma lacustre mitochondrion, comple... | 70 | 9e-13 |
| ref NC_001804.1 | Latimeria chalumnae mitochondrion, complet... | 68 | 4e-12 |
| ref NC_000880.1 | Vidua chalybeata mitochondrion, complete g... | 66 | 1e-11 |
| ref NC_002069.1 | Corvus frugilegus mitochondrion, complete ... | 64 | 6e-11 |
| ref NC_000886.1 | Chelonia mydas mitochondrial DNA, complete... | 62 | 2e-10 |
| ref NC_001646.1 | Pongo pygmaeus mitochondrion, complete genome | 62 | 2e-10 |
| ref NC_001606.1 | Cyprinus carpio mitochondrion, complete ge... | 62 | 2e-10 |
| ref NC_000890.1 | Mustelus manazo mitochondrion, complete ge... | 60 | 9e-10 |
| ref NC_001323.1 | Gallus gallus mitochondrion, complete genome | 50 | 9e-10 |
| ref NC_002079.1 | Carassius auratus mitochondrion, complete ... | 58 | 3e-09 |
| ref NC_000934.1 | Loxodonta africana mitochondrion, complete... | 56 | 1e-08 |
| ref NC_000878.1 | Falco peregrinus mitochondrion, complete g... | 56 | 1e-08 |
| ref NC_000846.1 | Rhea americana mitochondrion, complete genome | 56 | 1e-08 |
| ref NC_002196.1 | Ciconia boyciana mitochondrion, complete g... | 54 | 5e-08 |
| ref NC_001960.1 | Salmo salar mitochondrion, complete genome | 54 | 5e-08 |
| ref NC_001778.1 | Polypterus ornatipinnis mitochondrion, com... | 54 | 5e-08 |
| ref NC_002083.1 | Pongo pygmaeus abelii mitochondrion, compl... | 52 | 2e-07 |
| ref NC_001953.1 | Struthio camelus complete mitochondrial ge... | 52 | 2e-07 |
| ref NC_001947.1 | Pelomedusa subrufa mitochondrion, complete... | 52 | 2e-07 |
| ref NC_001770.1 | Arbacia lixula mitochondrion, complete genome | 52 | 2e-07 |

Alignments

| | | | |
|-----------|-------|---|-------|
| cmpseq_0 | 1 | tgaatctgaggaggtctctcagtagacaaagctaccctgacacgattctcttgccctccac | 60 |
| NC_001700 | 15524 |g..g.....c.....a.....g..... | 15581 |
| NC_001325 | 15580 |a..t.....t.....a..t..a.....c..... | 15619 |
| NC_002008 | 14673 |c.....g.....a.....a.....a.....t..... | 14729 |
| NC_001602 | 15553 |a..t.....t.....a..t..a..g.....c..... | 15612 |
| NC_000884 | 14650 |g..g.....c.....a..... | 14709 |
| NC_001808 | 14662 |a..t..c..t.....c..a..t.....c.....t..... | 14721 |
| NC_001892 | 14654 |t.....c.....c.....t..a..c.....c.....t..... | 14713 |
| NC_001788 | 14671 |t..c..a.....c.....c.....c.....t..... | 14716 |
| NC_002078 | 14663 |c.....t.....t.....a..a..a.....c..... | 14716 |
| NC_001821 | 14657 |a.....t..a.....c.....c..... | 14723 |
| NC_001779 | 14664 |a.....c.....c.....c.....c.....c..... | 14684 |
| NC_001569 | 14625 |t.....g.....t.....c.....c.....c.....c..... | 14717 |
| NC_000889 | 14658 |t.....c.....c.....c.....c.....c.....t..... | 14711 |
| NC_001640 | 14674 |t..a.....c.....t..c.....c.....c.....t..... | 14727 |
| NC_001774 | 14670 |g..a.....c.....c.....c.....c.....c.....t..... | 14727 |

| | | | |
|-----------|-------|--|-------|
| NC_000845 | 15828 |g....t.c.c.....a....c.....c..... | 15887 |
| NC_001665 | 14610 |a....a....c.....c.a..... | 14669 |
| NC_001567 | 15000 |c.a.....a....t.c.....c.t....t | 15059 |
| NC_001643 | 14655 |a.....gcc.....t.....ca..... | 14710 |
| NC_001941 | 14645 |g....a.....c.c.....c.....t.. | 14704 |
| NC_002191 | 14671 | ...t...t.g.....g.a.c.....c..... | 14730 |
| NC_001913 | 14661 |a.t....t.c.....c.t.c.....c.t.c. | 14720 |
| NC_001644 | 14656 |a.....gcc.....t.....ca.c.... | 14711 |
| NC_001807 | 15233 |a.....gtc.c.....c.....a....t.. | 15292 |
| NC_001601 | 15096 |c.t.c.t.g.t.....a.a.a....c..... | 15155 |
| NC_002009 | 14636 |t....t.c.....a.t.c.c.....c.....t | 14695 |
| NC_001645 | 14686 |t.....a..... | 14714 |
| NC_001321 | 15099 |c.c....t....t.....a.a.a....c.t....t.. | 15158 |
| NC_001610 | 14663 | ...t....a....c.t....t.....a.a.c....t....t.c. | 14722 |
| NC_002082 | 14657 |c....a.....t.c.c.a.c....c.t.ca....t.. | 14712 |
| NC_001727 | 15764 |g.g.....t.a.t.....g.....c..... | 15823 |
| NC_001804 | 14829 |t.t.c.....c.c.a.c.g..... | 14888 |
| NC_000880 | 15477 |a..... | 15500 |
| NC_002069 | 14190 | ...t.a.....cc.c.a.a.c..... | 14243 |
| NC_000886 | 14718 |g.c.....t.a....a.c.....ca..... | 14777 |
| NC_001646 | 14716 |a.c.t.... | 14736 |
| NC_001606 | 15779 | ...t.g.....t.a.a.a....c.a..... | 15838 |
| NC_000890 | 14841 |g.t.....c.c....t....c.t....t.. | 14900 |
| NC_002079 | 15782 | ...t.....c....t.t.a.at.a....c.a.t.... | 15841 |
| NC_000934 | 14633 |t.....t.....a.t.a.at....t.c...c....t | 14692 |
| NC_000878 | 14222 |cc.a.a....c.....c...c.a.... | 14263 |
| NC_000846 | 14145 |cc.....a.c.....c...c.s.... | 14186 |
| NC_001960 | 15870 | ...t.....a.t.t....c.c....a....t.c..... | 15929 |
| NC_001778 | 14763 |g.t....t.t....c.a.a.t.c.....a.... | 14822 |
| NC_001953 | 14115 |c.a....t....cc.c....a.....c.t.... | 14169 |
| NC_001947 | 14805 |a.t....t.a....a.c..... | 14854 |
| NC_001770 | 15069 | ...t....t.....a....a.c.....t.t.... | 15119 |

| tempseq_0 | 61 | ttcatcctccatttaccatcttcagcttcagcagcagctccacctccctattcccttcacgag | 120 |
|-----------|-------|---|-------|
| NC_001700 | 15584 |c.t.....c.t.....ct.....g...a.....t.....t..a | 15643 |
| NC_001325 | 15640 |a.....cg.ag.a.t..a...ac.....a.....a.....a | 15699 |
| NC_002008 | 14730 |c.t.c.....g.....at..a.....t..a.....a | 14789 |
| NC_001602 | 15613 |a.....cg.ag.a.t..a.....a.....a.....a | 15672 |
| NC_000884 | 14710 | ..t..t.....c.....a.c.c.....cgat.....t.....c..... | 14769 |
| NC_001808 | 14722 | ..t.....c.c.....t...ac..c.....atcac.....a.....a | 14781 |
| NC_001892 | 14714 | ..t..t..a..c.c.t..cg...c.....t.at.....c.....a | 14773 |
| NC_001788 | 14731 | ..t..t..a..c.....a.....c.g.t.atc.....t..a.....c.....a | 14790 |
| NC_002078 | 14717 | ..t.....g.....t..cg.....tat.....t..a.....t..a.....a | 14776 |
| NC_001821 | 14717 |t.a.....t.....a...a.c.t.t.....gt.....a.....a | 14776 |
| NC_001779 | 14724 | ..t.....c.c.t...ct..c.....a..c.....a.....a.....a | 14783 |

| NC | 001569 | 14685 |c.a.....t...g.g.c.....acc..t.....c.....a | 14744 |
|----|--------|-------|---|-------|
| NC | 000889 | 14718 | ..t..c.....cg.t..a...a...catc.....t..a.....c..t..a | 14777 |
| NC | 001640 | 14734 |a..c..c.....a...c..g..t..tc..a..t..a.....t.....a | 14793 |
| NC | 001794 | 14730 | ..t.....a.....c.....a...c.....t..ct..t.....a..... | 14789 |
| NC | 001794 | 14462 |a.....c.....a...c.....t..ct..t.....a..... | 14475 |
| NC | 000845 | 15888 | ..t.....g.....c.....ta.c.c.c.....c..a..t.....g.....a | 15947 |
| NC | 001665 | 14670 |c.....c..t...g.c.c.c.....acc..a..t..t..t.....c.....a | 14729 |
| NC | 001567 | 15060 | ..t.....c.....ac..ad..t..cat.....a.....c.....a | 15119 |
| NC | 001643 | 14711 | ..t..t..a..c..c.....a...c.....a..a..c..t..t.....t..a.....a | 14770 |
| NC | 001941 | 14705 | ..t..tc.c.....c.....g.....c..c..cat..t.....a..c.....c.....a | 14764 |
| NC | 002391 | 14731 |t..g.....t..tg.g..a.....tg..t.....gt.....c.....a | 14790 |
| NC | 001913 | 14721 |t.g.....a.....c.....a..a..c..t..t.....t.....a | 14771 |
| NC | 001644 | 14712 | ..t.....a..c..c..t...a...c.....a..a..c..t..t.....t.....a | 15352 |
| NC | 001807 | 15293 |t.g..c..c..c..t..tg.....c.....a..c.....t..g.....a | 15215 |
| NC | 001601 | 15156 |t..c..c..c.....cat..at.....acc.....a..c.....t.....a | 14755 |
| NC | 002009 | 14596 | ..tc.a.....c..c..tg..a.....t..ac.....cc.....t..a.....a | 14774 |
| NC | 001645 | 14715 | ..t.....a..c..c.....a.....a.....a..cc.....t.....t..a.....a | 15218 |
| NC | 001331 | 15159 | ..t.....c..c..c.....ct..at.....acc.....ca..t.....t.....a | 14782 |
| NC | 001610 | 14723 | ..c..t.....c.....c..t...a...t..c..a..t..t.....t.....t.....a | 14772 |
| NC | 002063 | 14713 |a..t..c..t...a.g..c.....cc.g.....t.....a..... | 15826 |
| NC | 001727 | 15824 |a.....c.....a.....c.....a.....c.....a..... | 15843 |
| NC | 001727 | 15872 |a.....c.....a.....c.....a.....c.....a..... | 14702 |
| NC | 001904 | 14887 |c.....g..... | |

| | | | |
|-----------|-------|--|-------|
| | |g..c.....t... | 14948 |
| NC_001804 | 14928 | | |
| NC_000880 | 15567 |ac.....a | 15591 |
| NC_002069 | 14244 | ...c....a..C...g.a...g...gc...a..cc...t.....aaCC.....a | 14303 |
| NC_000886 | 14778 | ... | 14780 |
| NC_001646 | 14737 |a..a..t..C.....Ca.....a..a.CC.t.....a | 14796 |
| NC_001606 | 15839 | ... | 15841 |
| NC_000890 | 14901 | .. | 14902 |
| NC_002079 | 15842 | ...C....a..... | 15862 |
| NC_000934 | 14693 |t..... | 14708 |
| NC_000878 | 14264 | ...C.a..... | 14277 |
| NC_000846 | 14235 |a.....a | 14246 |
| NC_000846 | 14187 | ... | 14189 |
| NC_001960 | 15930 | ... | 15932 |
| NC_001778 | 14823 |t..... | 14833 |
| NC_001953 | 14170 | ...C....C..... | 14184 |
| NC_001770 | 15120 | ... | 15122 |

| tmpseq_0 | 121 | acaggatcctaacaacccccccaggaatagatccgactcagacaaaattccattccaccca | 15703 |
|-----------|-------|---|-------|
| NC_001700 | 15644 |tac.....c.....g | 15759 |
| NC_001325 | 15700 |a.....c.....ca.....c.....t | 14849 |
| NC_002008 | 14790 | ..c....c.....c.....cac...a.....c.....g | 15732 |
| NC_001602 | 15673 |a.....c.....ca..c.....c.....t | 14829 |
| NC_000884 | 14770 |a.....a.....c..aac..a.....c.....c | 14841 |
| NC_001808 | 14782 |c..t.....a.....ccc...a..at.....c.....t | 14833 |
| NC_001892 | 14774 |g..t.....a.....t..aac..a..a.....c.....g | 14850 |
| NC_001788 | 14791 |c.....c.....ccc...t..at.....c.....t | 14836 |
| NC_002078 | 14777 |t..t.....t..a..t..t.....c.....g | 14836 |
| NC_001821 | 14777 |a.....a.....t..ctcg..aa..at.....c.....t | 14843 |
| NC_001779 | 14784 |g..c.....a.....tcc...a..at.....c.....c | 14804 |
| NC_001569 | 14745 |a.....aa.....t..aac..a..tg.....t.....c | 14837 |
| NC_000889 | 14778 |c.....aa.....cccc..aa..g.....c.....c | 14853 |
| NC_001640 | 14794 |t.....c.....ccc...tatg.....c.....t | 14849 |
| NC_001794 | 14790 | ..c..t.....a..t.....caacc.....c.....c | 16007 |
| NC_000845 | 15948 | ..c....c.....ta..c.....ctc...a..at.....t.....t | 14789 |
| NC_001665 | 14730 |a..t.....a.....t..aac.....g.....c.....c | 15179 |
| NC_001567 | 15120 |c..c.....aa.....tccc..a..gt.....c.....c | 14830 |
| NC_001643 | 14771 |a..t.....c.....cacc...c....c.....a..c.....c | 14824 |
| NC_001941 | 14765 |c.....a.....tcc...g..a.....t.....c.....t | 14814 |
| NC_002391 | 14791 |a.....a.....t.....c.....c.....c | 14840 |
| NC_001913 | 14815 |a..t.....ct.....cacc...c....c.....a..c.....c | 14811 |
| NC_001644 | 14772 |g....a.....ct.....cacc...c..t..c.....ca..c.....t | 15412 |
| NC_001807 | 15353 |c.....a.....c..ccc...t..at.....t.....c | 15275 |
| NC_001601 | 15216 |a.....c..tcc...a.....c.....t.....c | 14815 |
| NC_002009 | 14756 |a.....tcc...c..cccc..a.....t.....ca..c.....c | 14814 |
| NC_001545 | 14775 |c.....a.....c..ccc...at.....t.....c | 15278 |
| NC_001321 | 15219 |a.g...t..aa.....cc...a.....t.....c | 14842 |

[illegible][illegible]

NC_000884 14830 ..t..... 14846
NC_001808 14842c.....aa..t..c.c.....ac.cgcc..a 14901
NC_001892 14834 ..t.....t.....c..a.....a..cc....c..tt.tccc.....acc..a 14893
NC_001788 14851t.....c.....a..a..... 14882
NC_001788 15080 15095
NC_002078 14837 14853
NC_001821 14837t.....t..... 14859
NC_001779 14844c..... 14866
NC_001569 14805t..... 14827
NC_000889 14838 ..t.....g..c..... 14860
NC_001640 14854 ..t..t.....t.....c..... 14876
NC_001640 15085 15098
NC_001794 14850 ..t..t..t..... 14867
NC_000845 16008t..... 16024
NC_001665 14790 ..t..t.....t..... 14806
NC_001567 15180t..c..t..g..c..t.....c.....t.....t..a.....a 15239

ag

NC_001643 14831 14853
NC_001941 14825 ..t.....c..t.....c..... 14847
NC_001913 14841 14857
NC_001644 14832c..... 14854
NC_001807 15413 15429
NC_001601 15276t..... 15292
NC_002009 14816t..t..t..... 14835
NC_001645 14835c.....a..... 14863
NC_001321 15279 ...c.....t..... 15295
NC_001610 14843t..c..a..... 14865
NC_002082 14833t.....c..... 14855
NC_001727 15944 15947
NC_000880 15652 15659
NC_002069 14364t..... 14381
NC_001323 15562t..ct.....c..t..... 15588
NC_002079 15962 15965
NC_000934 14813 14817
NC_000878 14384t..tc..... 14406
NC_000846 14307 14310
NC_002196 16392t..t..cc.....a..... 16421
NC_002083 14867c.....a..... 14895
NC_001953 14290 14293

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NC_001700 15764t.....c.....a..c.....a.....t.. 15823
NC_001325 15820 ..g.....c.....a..c.....t..... 15867
NC_002008 14914t.....c.....a.....a.....c.....a.....c... 14969
NC_001602 15793 ..a.....t.....a..g.....c.....t..c... 15852
NC_000884 14900c.....a.....a.....ca..c.....g..g 14949
NC_001808 14902 ..t.....a..cc.....t..c.....c.....t..... 14960
NC_001892 14894 ..t.....c.....t..a.....c.....c.....a... 14953
NC_002078 14909a..... 14928
NC_000845 16071ac.....a..c.....c...a..a.....a... 16127
NC_001567 15240 ..a.....g...c.....cc.c.....a.....c..a..... 15292
NC_001913 14901t.....a.....a..c.....c.....c..t 14960
NC_001644 1484 1492
NC_001807 15476cc....c.....a..c..t..t..c..ca.....ct.. 15532
NC_002009 14880t.....cc.....a..c..t..t..t..a..a..c..a..t 14935
NC_001645 14898cc.....a..c.....c..t..a.....c... 14954
NC_001610 14907t..t.....t..c..t..c..a..t..t..c..t 14962
NC_002082 14950 14952
NC_001804 15071a..t..a.....a..... 15108
NC_000886 14980a..c.....t..ca..a..... 15017
NC_002196 16454ca...ac...t.....a..g...t..c..a..... 16507
NC_001950 16155c..... 16169

cmpseq_0 301 aatccccctccccctacccaagcctgaat 328
NC_001700 15824t..a..... 15871
NC_002008 14970 ..c.....a.....t..... 14975
NC_001602 15833 ..gc.....a..... 15872
NC_000884 14950 14954
NC_001922 14754 ..g..... 14770

| | | | |
|------------------|-------|------------------------|-------|
| <u>NC 001779</u> | 3081 | | 3094 |
| <u>NC 000845</u> | 16128 | ..c.....a..... | 16144 |
| <u>NC 001911</u> | 14961 | | 14980 |
| <u>NC 001644</u> | 1491 | ...c..... | 1501 |
| <u>NC 001807</u> | 15533 | ..c.....c.....c.... | 15560 |
| <u>NC 002009</u> | 14936 |c.....a.... | 14963 |
| <u>NC 001645</u> | 14955 | .gc.....a.....c.... | 14974 |
| <u>NC 001610</u> | 14963 | ..c.....g..c.....a.... | 14990 |
| <u>NC 002082</u> | 14953 | ..c.....c..... | 14972 |
| <u>NC 001960</u> | 16170 | gt...t..a..t..... | 16197 |
| <u>NC 001951</u> | 14416 |c.... | 14437 |

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129


| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Gapped

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 788
 Number of Sequences: 129
 Number of extensions: 788
 Number of successful extensions: 168
 Number of sequences better than 10.0: 77
 length of query: 328
 length of database: 3,164,247
 effective HSP length: 15
 effective length of query: 313
 effective length of database: 3,162,312
 effective search space: 989803656
 effective search space used: 989803656
 T: 0
 A: 30
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 14 (28.2 bits)

Table 4


BLASTN 2.1.2 [Nov-13-2000]Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122


Query-

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 50 Blast Hits on the Query Sequence
Mouse-over to show define and scores. Click to show alignments

Sequences producing significant alignments:

| | | Score (bits) | E Value |
|------------------------|---|-----------------|------------|
| gb AY005809.1 | Panthera pardus cytochrome b gene, partial c... | 603 | e-170 |
| gb AF051054.1 AF051054 | Panthera tigris sumatrae isolate Su1... | 527 | e-147 |
| gb AF051053.1 AF051053 | Panthera tigris tigris isolate B7 mi... | 527 | e-147 |
| gb AF051050.1 AF051050 | Panthera tigris corbetti isolate C2 ... | 476 | e-132 |
| gb AF051049.1 AF051049 | Panthera tigris corbetti isolate C1 ... | 476 | e-132 |
| gb AF051025.1 AF051025 | Panthera tigris tigris isolate B9 cy... | 450 | e-127 |
| gb AF051024.1 AF051024 | Panthera tigris tigris isolate B8 cy... | 450 | e-127 |
| gb AF051023.1 AF051023 | Panthera tigris tigris isolate B7 cy... | 450 | e-127 |
| gb AF051022.1 AF051022 | Panthera tigris tigris isolate B6 cy... | 450 | e-127 |
| gb AF051021.1 AF051021 | Panthera tigris tigris isolate B5 cy... | 450 | e-127 |
| gb AF051018.1 AF051018 | Panthera tigris tigris isolate B2 cy... | 450 | e-127 |
| gb AF051051.1 AF051051 | Panthera tigris corbetti isolate C3 ... | 452 | e-125 |
| gb AF051048.1 AF051048 | Panthera tigris sumatrae isolate Su1... | 452 | e-125 |
| gb AF051047.1 AF051047 | Panthera tigris sumatrae isolate Su9... | 452 | e-125 |
| gb AF051046.1 AF051046 | Panthera tigris sumatrae isolate Su7... | 452 | e-125 |
| gb AF051045.1 AF051045 | Panthera tigris sumatrae isolate Su6... | 452 | e-125 |
| gb AF051044.1 AF051044 | Panthera tigris sumatrae isolate Su5... | 452 | e-125 |
| gb AF051042.1 AF051042 | Panthera tigris sumatrae isolate Su3... | 452 | e-125 |
| gb AF051041.1 AF051041 | Panthera tigris sumatrae isolate Su2... | 452 | e-125 |
| gb AF051040.1 AF051040 | Panthera tigris sumatrae isolate Su1... | 452 | e-125 |
| gb AF051039.1 AF051039 | Panthera tigris altaica isolate S15 ... | 452 | e-125 |
| gb AF051038.1 AF051038 | Panthera tigris altaica isolate S14 ... | 452 | e-125 |
| gb AF051037.1 AF051037 | Panthera tigris altaica isolate S13 ... | 452 | e-125 |
| gb AF051036.1 AF051036 | Panthera tigris altaica isolate S12 ... | 452 | e-125 |
| gb AF051035.1 AF051035 | Panthera tigris altaica isolate S11 ... | 452 | e-125 |
| gb AF051034.1 AF051034 | Panthera tigris altaica isolate S10 ... | 452 | e-125 |
| gb AF051033.1 AF051033 | Panthera tigris altaica isolate S8 c... | 452 | e-125 |
| gb AF051032.1 AF051032 | Panthera tigris altaica isolate S7 c... | 452 | e-125 |
| gb AF051031.1 AF051031 | Panthera tigris altaica isolate S6 c... | 452 | e-125 |
| gb AF051030.1 AF051030 | Panthera tigris altaica isolate S5 c... | 452 | e-125 |
| gb AF051029.1 AF051029 | Panthera tigris altaica isolate S4 c... | 452 | e-125 |
| gb AF051028.1 AF051028 | Panthera tigris altaica isolate S3 c... | 452 | e-125 |
| gb AF051027.1 AF051027 | Panthera tigris altaica isolate S2 c... | 452 | e-125 |
| gb AF051026.1 AF051026 | Panthera tigris altaica isolate S1 c... | 452 | e-125 |
| gb AF051020.1 AF051020 | Panthera tigris tigris isolate B4 cy... | 452 | e-125 |
| gb AF051019.1 AF051019 | Panthera tigris tigris isolate B3 cy... | 444 | e-122 |
| gb AF051043.1 AF051043 | Panthera tigris sumatrae isolate Su4... | 444 | e-122 |
| emb X82301.1 M1PTCYTB | P.tigris mitochondrial cytochrome b gene | 440 | e-121 |
| gb AF051052.1 AF051052 | Panthera leo cytochrome b (cytb) gen... | 438 | e-121 |
| emb X82300.1 M1PLCYTBG | P.leo mitochondrial cytochrome b gene | 399 | e-106 |
| gb AB004238.1 AB004238 | Felis catus mitochondrial DNA for c... | 381 | e-103 |
| gb AB004237.1 AB004237 | Felis catus mitochondrial DNA for c... | 377 | e-102 |
| emb X82296.1 M1FDCTB | F.domesticus mitochondrial cytochrome... | 365 | 1e-98 |
| gb NC 001700.1 | Felis catus mitochondrion, complete genome | 365 | 1e-98 |
| gb U20751.1 FCU20751 | Felis catus mitochondrion, complete ge... | 276 | 7e-72 |
| gb AF125145.1 AF125145 | Viverricula indica cytochrome b gene... | 270 | 4e-70 |
| gb AF125144.1 AF125144 | Chrotogale owstoni cytochrome b gene... | 255 | 7e-66 |
| gb AF154975.1 AF154975 | Martes martes specimen_voucher AF175... | 256 | 7e-66 |
| gb AB051237.1 AB051237 | Martes martes mitochondrial cytb ge... | 246 | 6e-63 |
| gb AF125149.1 AF125149 | Viverra zangalunga cytochrome b gene... | | |

Alignments

| | | | |
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| cmpseq_0 | 1 | tgaatccgaggaggctcttcagtagacaaagctaccccgacacgattctcttcgctctccac | 60 |
| AY005809 | 39 |g.....c..... | 98 |
| AF051054 | 487 |g.....c..... | 546 |
| AF051053 | 487 |g.....c..... | 546 |
| AF051050 | 487 |g.....c..... | 546 |
| AF051049 | 487 |g.....c..... | 546 |
| AF051025 | 487 |g.....c..... | 546 |
| AF051024 | 487 |g.....c..... | 546 |
| AF051023 | 487 |g.....c..... | 546 |
| AF051022 | 487 |g.....c..... | 546 |
| AF051021 | 487 |g.....c..... | 546 |
| AF051018 | 487 |g.....c..... | 546 |
| AF051051 | 487 |g.....c..... | 546 |
| AF051048 | 487 |g.....c..... | 546 |
| AF051047 | 487 |g.....c..... | 546 |

| | | | |
|------------------|-------|---|-------|
| <u>AF053046</u> | 487 |g..t..... | 546 |
| <u>AF053045</u> | 487 |g..t..... | 546 |
| <u>AF053044</u> | 487 |g..t..... | 546 |
| <u>AF053042</u> | 487 |g..t..... | 546 |
| <u>AF053041</u> | 487 |g..t..... | 546 |
| <u>AF053040</u> | 487 |g..t..... | 546 |
| <u>AF053039</u> | 487 |g..t..... | 546 |
| <u>AF053038</u> | 487 |g..t..... | 546 |
| <u>AF053037</u> | 487 |g..t..... | 546 |
| <u>AF053036</u> | 487 |g..t..... | 546 |
| <u>AF053035</u> | 487 |g..t..... | 546 |
| <u>AF053034</u> | 487 |g..t..... | 546 |
| <u>AF053033</u> | 487 |g..t..... | 546 |
| <u>AF053032</u> | 487 |g..t..... | 546 |
| <u>AF053031</u> | 487 |g..t..... | 546 |
| <u>AF053030</u> | 487 |g..t..... | 546 |
| <u>AF053029</u> | 487 |g..t..... | 546 |
| <u>AF053028</u> | 487 |g..t..... | 546 |
| <u>AF053027</u> | 487 |g..t..... | 546 |
| <u>AF053026</u> | 487 |g..t..... | 546 |
| <u>AF053020</u> | 487 |g..t..... | 546 |
| <u>AF053019</u> | 487 |g..t..... | 546 |
| <u>AF053043</u> | 487 |g..t..... | 546 |
| <u>X82301</u> | 487 |g..t..... | 546 |
| <u>AF053052</u> | 487 |c..... | 546 |
| <u>X82300</u> | 490 |c..... | 546 |
| <u>A8004238</u> | 487 |g.....c.....a..... | 546 |
| <u>A3004237</u> | 487 |g.....c.....a.....t..... | 546 |
| <u>X82296</u> | 487 |g.....c.....a..... | 546 |
| <u>NC 001700</u> | 15524 |g..g.....c.....a.....g..... | 15583 |
| <u>U20753</u> | 15524 |g..g.....c.....a.....g..... | 15583 |
| <u>AF125145</u> | 357 |t.....t.....c.....t.a..c.....c..... | 416 |
| <u>AF125144</u> | 357 |t.....g.....t.....t.....c.....a.....c..... | 416 |
| <u>AF154975</u> | 487 |g.....g.....c.....a..g.....c..... | 546 |
| <u>A3051237</u> | 487 |g.....g.....c.....a..g.....c..... | 546 |
| <u>AF125149</u> | 357 |g.....t.....g.....c.....t.a.....t..... | 416 |
| <u>cmpseq_0</u> | 61 | ttcatccttccatttatcatcttcagctcttagcagcagtcacccctcctattccttcacgag | 120 |
| <u>AY005809</u> | 99 |c..... | 158 |
| <u>AF053054</u> | 547 |c.....c..t... | 606 |
| <u>AF053053</u> | 547 |c.....c..t... | 606 |
| <u>AF053050</u> | 547 |g.....c.....a | 606 |
| <u>AF053049</u> | 547 |g.....c.....a | 606 |
| <u>AF053025</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053024</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053023</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053022</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053021</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053018</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053051</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053048</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053047</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053046</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053045</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053044</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053042</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053041</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053040</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053039</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053038</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053037</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053036</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053035</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053034</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053033</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053032</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053031</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053030</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053029</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053028</u> | 547 |g.....g.....c.....a | 606 |
| <u>AF053027</u> | 547 |g.....g.....c.....a | 606 |

[illegible]

| | | | |
|-----------|-------|---|-------|
| AY005809 | 219 |c..... | 278 |
| AF051054 | 667 |c.....a..... | 726 |
| AF051053 | 667 |c.....a..... | 726 |
| AF051050 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051049 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051025 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051024 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051023 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051022 | 667 |c.....t.a.....cc.....a.c..... | 726 |
| AF051021 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051018 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051051 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051048 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051047 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051046 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051045 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051044 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051042 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051041 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051040 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051039 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051038 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051037 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051036 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051035 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051034 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051033 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051032 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051031 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051030 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051029 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051028 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051027 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051026 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051020 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051019 | 667 |c.....t.a.....cc.....a.c.....c..... | 726 |
| AF051043 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| X82301 | 667 |c.....t.a.....cc.....g.....a.c..... | 726 |
| AF051052 | 667 |c.....a.....t.....t.....a..... | 726 |
| X82300 | 667 |c.....a.....t.....t.....a..... | 726 |
| AB004238 | 667 |c.....c.....a.....t.....g.....cc.....a..... | 726 |
| AB004237 | 667 |c.....c.....a.....t.....g.....cc.....a..... | 726 |
| X82296 | 667 |c.....c.....a.....t.....g.....cc.....a..... | 15763 |
| NC_001700 | 15704 |c.....c.....a.....t.....g.....cc.....a..... | 15763 |
| U20753 | 15704 |c.....c.....a.....t.....g.....cc.....a..... | 596 |
| AF125145 | 537 |c.....c.....a.....t.....g.....cc.....a..... | 596 |
| AF125144 | 537 |c.....c.....a.....t.....g.....cc.....a..... | 726 |
| AF154975 | 667 |c.....c.....a.....t.....g.....cc.....a..... | 726 |
| AB051237 | 667 |c.....c.....a.....t.....g.....cc.....a..... | 596 |
| AF125149 | 537 |c.....c.....a.....t.....g.....cc.....a..... | 596 |
| cmpseq_0 | 241 | gtccctattctccaccagacctgtcaggagaccccgataactacatccctgcgaacccctcta | 100 |
| AY005809 | 279 |c.....c.....c..... | 338 |
| AF051054 | 727 |a.....g.....c..... | 786 |
| AF051053 | 727 |a.....g.....c..... | 786 |
| AF051050 | 727 |a.....c.....c..... | 786 |
| AF051049 | 727 |a.....c.....c..... | 786 |
| AF051025 | 727 |a.....c.....c..... | 786 |
| AF051024 | 727 |a.....c.....c..... | 786 |
| AF051023 | 727 |a.....c.....c..... | 786 |
| AF051022 | 727 |a.....c.....c..... | 786 |
| AF051021 | 727 |a.....c.....c..... | 786 |
| AF051018 | 727 |a.....c.....c..... | 786 |
| AF051051 | 727 |a.....c.....c..... | 786 |
| AF051048 | 727 |a.....c.....c..... | 786 |
| AF051047 | 727 |a.....c.....c..... | 786 |
| AF051046 | 727 |a.....c.....c..... | 786 |
| AF051045 | 727 |a.....c.....c..... | 786 |
| AF051044 | 727 |a.....c.....c..... | 786 |
| AF051043 | 727 |a.....c.....c..... | 786 |
| AF051042 | 727 |a.....c.....c..... | 786 |
| AF051041 | 727 |a.....c.....c..... | 786 |
| AF051040 | 727 |a.....c.....c..... | 786 |
| AF051039 | 727 |a.....c.....c..... | 786 |
| AF051038 | 727 |a.....c.....c..... | 786 |

| | | | |
|------------------|-------|---|-------|
| <u>AF053040</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053039</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053038</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053037</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053036</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053035</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053034</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053033</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053032</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053031</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053030</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053029</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053028</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053027</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053026</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053020</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053019</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053043</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>X82301</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>AF053052</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>X82300</u> | 727 |a.....c.....c.....c.....c..... | 786 |
| <u>A3004238</u> | 727 |c.....c.....a..c.g.....a.....c..... | 786 |
| <u>A3004237</u> | 727 |c.....c.....a..c.....a.....c..... | 786 |
| <u>X82296</u> | 727 |c.....c.....a..c.....a.....c..... | 786 |
| <u>NC 001700</u> | 15764 |c.....c.....a..c.....a.....c..... | 15823 |
| <u>U20753</u> | 15764 |c.....c.....a..c.....a.....c..... | 15823 |
| <u>AF125145</u> | 597 |c.....c.....a.....c.....c..... | 650 |
| <u>AF125144</u> | 597 |c.....c.....a.....c.....c..... | 656 |
| <u>AF154975</u> | 727 | ..a.....c.....c.g.....a..c.....c.....a..c | 786 |
| <u>A3051237</u> | 727 | ..a.....c.....c.g.....a..c.....c.....a..c | 786 |
| <u>AF125149</u> | 597 |c.....c.....a.....c.....c..... | 656 |
| <u>cmpseq_0</u> | 301 | aatacccccccccatatcaagcctgaat | 328 |
| <u>AY005809</u> | 339 |c.....c.....c.....c.....c..... | 366 |
| <u>AF053054</u> | 787 | ..c.....c.....c.....c.....c..... | 808 |
| <u>AF053053</u> | 787 | ..c.....c.....c.....c.....c..... | 808 |
| <u>AF053050</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053049</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053025</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053024</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053023</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053022</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053021</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053018</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053051</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053048</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053047</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053046</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053045</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053044</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053042</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053041</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053040</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053039</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053038</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053037</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053036</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053035</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053034</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053033</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053032</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053031</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053030</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053029</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053028</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053027</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053026</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053020</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053012</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>AF053043</u> | 787 |c.....c.....c.....c.....c..... | 814 |
| <u>X82301</u> | 787 |c.....c.....c.....c.....c..... | 814 |

| | | | |
|------------------|-------|----------------|-------|
| <u>AF051052</u> | 787 | .gc.....a..... | 812 |
| <u>X82100</u> | 787 | .gc.....a..... | 814 |
| <u>AB004238</u> | 787 |c..a..... | 814 |
| <u>AB004237</u> | 787 |c..a..... | 814 |
| <u>X82296</u> | 787 |c..a..... | 814 |
| <u>NC 001700</u> | 15824 |c..a..... | 15851 |
| <u>U20753</u> | 15824 |c..a..... | 15851 |
| <u>AF125144</u> | 657 | ..c..... | 664 |
| <u>AF154975</u> | 787 | ..c..a..a..... | 803 |
| <u>AB051237</u> | 787 | ..c..a..a..... | 803 |
| <u>AF125149</u> | 657 | ..c..... | 664 |

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,861,827,885

Number of sequences in database: 807,597

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Gapped

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 460542

Number of Sequences: 807597

Number of extensions: 460542

Number of successful extensions: 22671

Number of sequences better than 10.0: 6487

length of query: 328

length of database: 2,861,827,885

effective HSP length: 20

effective length of query: 308

effective length of database: 2,847,675,945

effective search space: 877084191060

effective search space used: 877084191060

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

Table 5. Reference animals and the allocated code numbers included in the study

| SN. | Code number | Name of the animal | Zoological name |
|-----|-------------|--------------------|------------------------------------|
| 1 | bhz25t | Indian tiger | <i>Panthera tigris tigris</i> |
| 2 | bhz26t | Indian tiger | <i>Panthera tigris tigris</i> |
| 3 | bhz30t | Indian tiger | <i>Panthera tigris tigris</i> |
| 4 | bhz45t | Indian tiger | <i>Panthera tigris tigris</i> |
| 5 | bhz56t | Indian tiger | <i>Panthera tigris tigris</i> |
| 6 | bhz63t | Indian tiger | <i>Panthera tigris tigris</i> |
| 7 | bhz20wt | Indian white tiger | <i>Panthera tigris bengalensis</i> |
| 8 | bhz22wt | Indian white tiger | <i>Panthera tigris bengalensis</i> |
| 9 | bhz23wt | Indian white tiger | <i>Panthera tigris bengalensis</i> |
| 10 | bhz28wt | Indian white tiger | <i>Panthera tigris bengalensis</i> |
| 11 | gz1l | Normal leopard | <i>Panthera pardus</i> |
| 12 | gz2l | Normal leopard | <i>Panthera pardus</i> |
| 13 | gz3l | Normal leopard | <i>Panthera pardus</i> |
| 14 | gz21cl | Clouded leopard | <i>Neofelis nebulosa</i> |
| 15 | gz22cl | Clouded leopard | <i>Neofelis nebulosa</i> |
| 16 | darz14sl | Snow leopard | <i>Panthera uncia</i> |
| 17 | darz15sl | Snow leopard | <i>Panthera uncia</i> |
| 18 | darz16sl | Snow leopard | <i>Panthera uncia</i> |
| 19 | sbz22al | Asiatic lion | <i>Panthera leo persica</i> |
| 20 | sbz38al | Asiatic lion | <i>Panthera leo persica</i> |
| 21 | sbz39al | Asiatic lion | <i>Panthera leo persica</i> |
| 22 | humsk | Human | <i>Homo sapiens sapiens</i> |
| 23 | chimss | Chimpanzee | <i>Pan sp.</i> |

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

| | | |
|------------|--|-----|
| sbz22al | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 50 |
| sbz38al | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| sbz39al | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| adil.flesh | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC | 60 |
| gz1nl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC | 60 |
| gz2nl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC | 60 |
| gz3nl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz23wt | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz28wt | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz22wt | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz20wt | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz63t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz56t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz26t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz30t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz45t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| bhz25t | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| d=14sl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| d=15sl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| d=16sl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| gz21cl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| gz22cl | TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC | 60 |
| chimss | TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCCTACACGATTCTTCACCTTCCAC | 60 |
| humsk | TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTCCAC | 60 |
| ***** | | |
| sbz22al | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA | 120 |
| sbz38al | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA | 120 |
| sbz39al | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA | 120 |
| adil.flesh | TTTCATCCTTCCATTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| gz1nl | TTTCATCCTTCCATTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| gz2nl | TTTCATCCTTCCATTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| gz3nl | TTTCATCCTTCCATTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz23wt | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz28wt | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz22wt | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz20wt | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz63t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz56t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz26t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz30t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz45t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| bhz25t | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| d=14sl | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| d=15sl | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| d=16sl | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| gz21cl | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| gz22cl | TTTCATCCTTCCATTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCTCTCCAGAG | 120 |
| chimss | TTTATCTTACCCTTCAATATCACAGCCCTAACCAACCTTCATCTCTATTCTTACACGAA | 120 |
| humsk | TTTCATCTTGCCTTCAATATTGAGCCCTAGCAGCAGTCCACCTCCTATTCTTGCACGAA | 120 |
| | | |
| sbz22al | ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAA TTCCATTCCATCCA | 190 |
| sbz38al | ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAA TTCCATTCCATCCA | 190 |

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sbz39a1      ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAAATTCCATTCCATCCA 130
adil.flesh   ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCATTCCACCCA 130
g=1n1        ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCATTCCACCCA 130
g=2n1        ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
g=3n1        ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=23wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=28wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=22wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=20wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=63t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=56t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=26t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=30t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=45t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
bh=25t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
dz=14s1      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
dz=15s1      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
dz=16s1      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCATTCCACCCA 130
g=21c1       ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCCAGACAAAATTCATTCCACCCA 130
g=22c1       ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCCAGACAAAATTCATTCCACCCA 130
chimss       ACAGGATCAAATAACCCCTGGGAATCAGCTCCCACTCCGACAAAATTCATTCCACCCA 130
humsk        ACGGGATCAAACAACCCCTAGGAATCAGCTCCCACTCCGATAAAAATTCATTCCACCCA 130
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sbz22a1      TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
sbz38a1      TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
sbz39a1      TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
adil.flesh   TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
g=1n1        TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
g=2n1        TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
g=3n1        TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=23wt      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=28wt      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=22wt      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=20wt      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=63t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=56t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=26t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=30t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=45t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
bh=25t       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
dz=14s1      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
dz=15s1      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
dz=16s1      TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
g=21c1       TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
g=22c1       TACTATACAATCAAAGATATCCTAGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
chimss       TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
humsk        TACTACACAATCAAAGATATCCTGGGCCCTTCTAGTACTAATCTTAACTCATACTACTC 240
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sbz22a1      GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
sbz38a1      GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
sbz39a1      GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
adil.flesh   GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
g=1n1        GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
g=2n1        GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
g=3n1        GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300
bh=23wt      GTCCATTCTCACCAGACCTATTAGGAGATCCCGACAACCTATACCCCGCCCAATCTCTTA 300

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bhz28wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz22wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz20wt GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz63t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz56t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz26t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz30t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz45t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
bhz25t GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
dz14sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
dz15sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
dz16sl GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAAATAACATCCCCGCCAACCCCTCTA 300
gz21cl GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTGACAAATTACACTCCCCGCCAACCCCTCTA 300
gz22cl GTTCTATTCTCCCCAGACCTACTAGGAGACCCGTGACAAATTACACTCCCCGCCAACCCCTCTA 300
chimss AACTATTCTCACCAGACCTCTAGGGCGATCCAGACAATAACCTAGCTAACCCCTTA 300
humsk AACTATTCTCACCAGACCTCTAGGGCGATCCAGACAATAACCTAGCTAACCCCTTA 300

sbz22al AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz38al AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz39al AGCACCCCTCCCCATATCAAACCTGAAT 328
adil.flesh AATACCCCTCCCCATATCAAGCCTGAAT 328
gz1nl AATACCCCTCCCCATATCAAGCCTGAAT 328
gz2nl AATACCCCTCCCCATATCAAGCCTGAAT 328
gz3nl AATACCCCTCCCCATATCAAGCCTGAAT 328
bhz23wt AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz28wt AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz22wt AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz20wt AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz63t AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz56t AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz26t AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz30t AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz45t AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz25t AACACCCCTCCCCATATCAAGCGCGAAT 328
dz14sl AACACCCCTCCCCATATCAAGCCCGAAT 328
dz15sl AACACCCCTCCCCATATCAAGCCCGAAT 328
dz16sl AACACCCCTCCCCATATCAAGCCCGAAT 328
gz21cl AATACCCCTCCCCATATCAAGCCTGAAT 328
gz22cl AATACCCCTCCCCATATCAAGCCTGAAT 328
chimss AACACCCCACCCCACATTAAACCCGAAT 328
humsk AACACCCCTCCCCACATCAAGCCCGAAT 328

Table 7d

| Position | 273 | 276 | 279 | 282 | 284 | 285 | 287 | 288 | 291 | 294 | 297 | 298 | 302 | 303 | 309 | 315 | 318 | 321 | 323 | 324 |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| adll.flesh | C | T | C | C | T | C | C | T | C | C | T | C | A | T | T | T | C | G | C | T |
| gz1l | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . | . |
| gz21l | . | . | . | . | . | . | . | G | . | . | . | . | . | . | . | . | . | . | . | . |
| gz23l | . | . | . | . | . | . | . | G | . | . | . | . | . | . | . | . | . | . | . | . |
| bhz25t | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz26t | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz30t | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz45t | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz56t | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz20wt | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz22wt | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| bhz23wt | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | G | C |
| dz14sl | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | . | C |
| dz15sl | . | . | . | . | . | . | . | C | . | . | . | . | . | C | . | . | . | . | . | C |
| sbz22al | . | C | . | T | C | . | . | C | . | T | . | . | G | C | . | . | . | A | . | . |
| sbz38al | . | C | . | T | C | . | . | C | . | T | . | . | G | C | . | . | . | A | . | . |
| gz21cl | T | C | T | . | C | T | . | C | . | . | . | . | . | . | . | . | . | . | . | . |
| gz22cl | T | C | T | . | C | T | . | C | . | . | . | . | . | . | . | . | . | . | . | . |
| chlmss | A | C | A | T | C | A | T | A | T | C | T | C | A | C | A | C | A | A | C | C |
| humsk | A | C | A | T | C | A | T | A | T | C | T | C | A | C | A | C | A | A | C | C |

Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

| | bhz20wt | bhz25t | dz14sl | humsk | chlmss | sbz22al | gz1L | gz2L | gz3L | gz21cl | adil.flesh |
|------------|---------|--------|--------|-------|--------|---------|------|------|------|--------|------------|
| bhz20wt | | 100 | 99.1 | 81.7 | 78.7 | 93.3 | 95.1 | 95.4 | 95.4 | 89.6 | 95.4 |
| bhz25t | 100 | | 99.1 | 81.7 | 78.7 | 93.3 | 95.1 | 95.4 | 95.4 | 89.6 | 95.4 |
| dz14sl | 99.1 | 99.1 | | 81.4 | 78.4 | 93 | 94.8 | 95.1 | 95.1 | 89.3 | 95.1 |
| humsk | 81.7 | 81.7 | 81.4 | | 86.9 | 79.6 | 81.1 | 80.2 | 80.2 | 79 | 81.4 |
| chlmss | 78.7 | 78.7 | 78.4 | 86.9 | | 78.7 | 79.6 | 78.7 | 78.7 | 76.8 | 79.9 |
| sbz22al | 93.3 | 93.3 | 93 | 79.6 | 78.7 | | 92.1 | 92.4 | 92.4 | 89 | 92.4 |
| gz1L | 95.1 | 95.1 | 94.8 | 81.1 | 79.6 | 92.1 | | 98.5 | 98.5 | 89.3 | 99.7 |
| gz2L | 95.4 | 95.4 | 95.1 | 80.2 | 78.7 | 92.4 | 98.5 | | 100 | 88.1 | 98.2 |
| gz3L | 95.4 | 95.4 | 95.1 | 80.2 | 78.7 | 92.4 | 98.5 | 100 | | 88.1 | 98.2 |
| gz21cl | 89.6 | 89.6 | 89.3 | 79 | 76.8 | 89 | 89.3 | 88.1 | 88.1 | | 89.6 |
| adil.flesh | 95.4 | 95.4 | 95.1 | 81.4 | 79.9 | 92.4 | 99.7 | 98.2 | 98.2 | 89.6 | |

Table 10



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997).
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query-

(25 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

| | Score | E Value |
|---|-------|---------|
| gb AF231651.1 AF231651 Strongylura notata clone HB-82 cyto... | 50 | 2e-05 |
| gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto... | 50 | 2e-05 |
| ref NC_002672.1 Dinornis giganteus mitochondrion, complete... | 50 | 2e-05 |
| ref NC_002673.1 Emeus crassus mitochondrion, complete genome | 50 | 2e-05 |
| gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome... | 50 | 2e-05 |
| gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen... | 50 | 2e-05 |
| gb AY016015.1 Emeus crassus mitochondrion, complete genome | 50 | 2e-05 |
| gb AY016013.1 Dinornis giganteus mitochondrion, complete g... | 50 | 2e-05 |
| gb AY016014.1 Dromaius novaehollandiae mitochondrion, part... | 50 | 2e-05 |
| gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYTB) ... | 50 | 2e-05 |
| gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene... | 50 | 2e-05 |
| gb AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b ... | 50 | 2e-05 |
| gb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b ... | 50 | 2e-05 |
| gb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b ... | 50 | 2e-05 |
| gb AY005205.1 Poospiza hispaniolensis cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AY005204.1 Poospiza garleppi cytochrome b (cytb) gene, ... | 50 | 2e-05 |
| gb AY005203.1 Poospiza erythrophrys cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb AY005201.1 Poospiza boliviana cytochrome b (cytb) gene... | 50 | 2e-05 |
| gb AY005199.1 Poospiza alticola isolate 2 cytochrome b (cy... | 50 | 2e-05 |
| gb AY005198.1 Poospiza alticola isolate 1 cytochrome b (cy... | 50 | 2e-05 |
| gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...) | 50 | 2e-05 |
| gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ... | 50 | 2e-05 |
| gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome... | 50 | 2e-05 |
| gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome... | 50 | 2e-05 |
| gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1... | 50 | 2e-05 |
| gb AF243857.1 AF243857 Strongylura notata notata cytochrome... | 50 | 2e-05 |
| gb AF243856.1 AF243856 Strongylura notata forsythia cytochr... | 50 | 2e-05 |
| ref NC_001567.1 Bos taurus mitochondrion, complete genome | 50 | 2e-05 |
| gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M... | 50 | 2e-05 |
| gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M... | 50 | 2e-05 |
| gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge... | 50 | 2e-05 |
| gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cyto... | 50 | 2e-05 |
| gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cyto... | 50 | 2e-05 |
| gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge... | 50 | 2e-05 |
| gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro... | 50 | 2e-05 |
| gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro... | 50 | 2e-05 |
| gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro... | 50 | 2e-05 |
| gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro... | 50 | 2e-05 |
| gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro... | 50 | 2e-05 |
| gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro... | 50 | 2e-05 |
| gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro... | 50 | 2e-05 |
| gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro... | 50 | 2e-05 |
| gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro... | 50 | 2e-05 |
| gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro... | 50 | 2e-05 |
| gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro... | 50 | 2e-05 |
| gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro... | 50 | 2e-05 |
| gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro... | 50 | 2e-05 |
| gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro... | 50 | 2e-05 |
| gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro... | 50 | 2e-05 |
| gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro... | 50 | 2e-05 |
| gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 39925 cytochro... | 50 | 2e-05 |
| gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 39163 cytochro... | 50 | 2e-05 |
| gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 39162 cytochrom... | 50 | 2e-05 |
| gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15896 cytochr... | 50 | 2e-05 |
| gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15892 cytochr... | 50 | 2e-05 |
| gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15891 cytochro... | 50 | 2e-05 |
| gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15890 cytochr... | 50 | 2e-05 |
| gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15889 cytochr... | 50 | 2e-05 |
| gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15888 cytochr... | 50 | 2e-05 |

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

| SL. | Name | P, S/AFF | P, S/AFR |
|------------|---|-----------------|-----------------|
| 1 | Indian black buck (<i>Antelope cervicapra</i>) | 97, 58 | 96, 54 |
| 2 | Sheep (<i>Ovis</i> | 87, 53 | 96, 54 |
| 3 | Pig (<i>Sus scrofa</i>) | 87, 52 | 87, 41 |
| 4 | Fresh water dolphin (<i>Platanista gangetica</i>) | 86, 49 | 82, 47 |

Sequences producing significant alignments:

| | Score | E |
|---|--------|-------|
| | (bits) | Value |
| gb AF231651.1 AF231651 Strongylura notata clone HB-82 cytoc... | 50 | 2e-05 |
| gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto... | 50 | 2e-05 |
| ref NC_002672.1 Dinornis giganteus mitochondrion, complete... | 50 | 2e-05 |
| ref NC_002673.1 Emeus crassus mitochondrion, complete genome | 50 | 2e-05 |
| gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome... | 50 | 2e-05 |
| gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen... | 50 | 2e-05 |
| gb AY016015.1 Emeus crassus mitochondrion, complete genome | 50 | 2e-05 |
| gb AY016013.1 Dinornis giganteus mitochondrion, complete g... | 50 | 2e-05 |
| gb AY016014.1 Dromaius novaehollandiae mitochondrion, part... | 50 | 2e-05 |
| gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYT3) ... | 50 | 2e-05 |
| gb AF074594.1 AF074594 Baelophus bicolor cytochrome b gene... | 50 | 2e-05 |
| gb AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b ... | 50 | 2e-05 |
| gb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b ... | 50 | 2e-05 |
| gb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b ... | 50 | 2e-05 |
| gb AY005205.1 Poospiza hispaniolensis cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AY005204.1 Poospiza garleppi cytochrome b (cytb) gene, ... | 50 | 2e-05 |
| gb AY005203.1 Poospiza erythrophrys cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb AY005201.1 Poospiza boliviana cytochrome b (cytb) gene,... | 50 | 2e-05 |
| gb AY005199.1 Poospiza alticola isolate 2 cytochrome b (cy... | 50 | 2e-05 |
| gb AY005198.1 Poospiza alticola isolate 1 cytochrome b (cy... | 50 | 2e-05 |
| gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...) | 50 | 2e-05 |
| gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ... | 50 | 2e-05 |
| gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome... | 50 | 2e-05 |
| gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome... | 50 | 2e-05 |
| gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1... | 50 | 2e-05 |
| gb AF243857.1 AF243857 Strongylura notata notata cytochrome... | 50 | 2e-05 |
| gb AF243856.1 AF243856 Strongylura notata forsythia cytochr... | 50 | 2e-05 |
| ref NC_001567.1 Bos taurus mitochondrion, complete genome | 50 | 2e-05 |
| gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M... | 50 | 2e-05 |
| gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M... | 50 | 2e-05 |
| gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype... | 50 | 2e-05 |
| gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge... | 50 | 2e-05 |
| gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cytoc... | 50 | 2e-05 |
| gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cytoc... | 50 | 2e-05 |
| gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge... | 50 | 2e-05 |
| gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283637.1 AF283637 Elaphe obsoleta LSUMZ 45359 cytochro... | 50 | 2e-05 |
| gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro... | 50 | 2e-05 |
| gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro... | 50 | 2e-05 |
| gb AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro... | 50 | 2e-05 |
| gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro... | 50 | 2e-05 |
| gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro... | 50 | 2e-05 |
| gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro... | 50 | 2e-05 |
| gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro... | 50 | 2e-05 |
| gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro... | 50 | 2e-05 |
| gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro... | 50 | 2e-05 |
| gb AF283627.1 AF283627 Elaphe obsoleta LSUMZ 41186 cytochro... | 50 | 2e-05 |
| gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro... | 50 | 2e-05 |
| gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro... | 50 | 2e-05 |
| gb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro... | 50 | 2e-05 |
| gb AF283623.1 AF283623 Elaphe obsoleta LSUMZ 44451 cytochro... | 50 | 2e-05 |
| gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro... | 50 | 2e-05 |
| gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 37225 cytochro... | 50 | 2e-05 |
| gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 37163 cytochro... | 50 | 2e-05 |
| gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 37162 cytochrom... | 50 | 2e-05 |
| gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15896 cytochr... | 50 | 2e-05 |
| gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15893 cytochr... | 50 | 2e-05 |
| gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15891 cytochro... | 50 | 2e-05 |
| gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15890 cytochr... | 50 | 2e-05 |
| gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15889 cytochr... | 50 | 2e-05 |
| gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15888 cytochr... | 50 | 2e-05 |

| | | | |
|------------------------|---|----|-------|
| gb AF283612.1 AF283612 | Elaphe obsoleta LSUMZ H15884 cytochr... | 50 | 2e-05 |
| gb AF283611.1 AF283611 | Elaphe obsoleta LSUMZ H15031 cytochr... | 50 | 2e-05 |
| gb AF283610.1 AF283610 | Elaphe obsoleta LSUMZ H15030 cytochr... | 50 | 2e-05 |
| gb AF283609.1 AF283609 | Elaphe obsoleta CAS 169468 cytochrom... | 50 | 2e-05 |
| gb AF283608.1 AF283608 | Elaphe obsoleta LSUMZ H14782 cytochr... | 50 | 2e-05 |
| gb AF283607.1 AF283607 | Elaphe obsoleta LSUMZ H14781 cytochr... | 50 | 2e-05 |
| gb AF283606.1 AF283606 | Elaphe obsoleta LSUMZ H14724 cytochr... | 50 | 2e-05 |
| gb AF283605.1 AF283605 | Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283604.1 AF283604 | Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283603.1 AF283603 | Elaphe obsoleta cytochrome b gene, c... | 50 | 2e-05 |
| gb AF283602.1 AF283602 | Elaphe obsoleta LSUMZ H3388 cytochro... | 50 | 2e-05 |
| gb AF283601.1 AF283601 | Elaphe obsoleta LSUMZ H3385 cytochro... | 50 | 2e-05 |
| gb AF283600.1 AF283600 | Elaphe obsoleta LSUMZ H3384 cytochro... | 50 | 2e-05 |
| gb AF283599.1 AF283599 | Elaphe bairdi LSUMZ H3382 cytochrome... | 50 | 2e-05 |
| gb AF283598.1 AF283598 | Elaphe bairdi LSUMZ H3381 cytochrome... | 50 | 2e-05 |
| gb AF283597.1 AF283597 | Elaphe obsoleta LSUMZ H3379 cytochro... | 50 | 2e-05 |
| gb AF283596.1 AF283596 | Elaphe obsoleta LSUMZ 39616 cytochro... | 50 | 2e-05 |
| gb AF283595.1 AF283595 | Elaphe obsoleta LSUMZ H3376 cytochro... | 50 | 2e-05 |
| gb AF283594.1 AF283594 | Elaphe obsoleta LSUMZ H3345 cytochro... | 50 | 2e-05 |
| gb AF283593.1 AF283593 | Elaphe obsoleta LSUMZ H3309 cytochro... | 50 | 2e-05 |
| gb AF283592.1 AF283592 | Elaphe obsoleta LSUMZ H3306 cytochro... | 50 | 2e-05 |
| gb AF283591.1 AF283591 | Elaphe obsoleta LSUMZ H3276 cytochro... | 50 | 2e-05 |
| gb AF283590.1 AF283590 | Elaphe obsoleta LSUMZ H3246 cytochro... | 50 | 2e-05 |
| gb AF283589.1 AF283589 | Elaphe obsoleta LSUMZ H3212 cytochro... | 50 | 2e-05 |
| gb AF283588.1 AF283588 | Elaphe obsoleta LSUMZ H3209 cytochro... | 50 | 2e-05 |
| gb AF283587.1 AF283587 | Elaphe obsoleta LSUMZ H3206 cytochro... | 50 | 2e-05 |
| gb AF283586.1 AF283586 | Elaphe obsoleta LSUMZ H3191 cytochro... | 50 | 2e-05 |
| gb AF283585.1 AF283585 | Elaphe obsoleta LSUMZ H3190 cytochro... | 50 | 2e-05 |
| gb AF283584.1 AF283584 | Elaphe obsoleta LSUMZ H3189 cytochro... | 50 | 2e-05 |
| gb AF283583.1 AF283583 | Elaphe obsoleta LSUMZ H3188 cytochro... | 50 | 2e-05 |
| gb AF283582.1 AF283582 | Elaphe obsoleta LSUMZ H3186 cytochro... | 50 | 2e-05 |
| gb AF283581.1 AF283581 | Elaphe obsoleta LSUMZ H3169 cytochro... | 50 | 2e-05 |
| gb AF283580.1 AF283580 | Elaphe obsoleta CAS 203083 cytochrom... | 50 | 2e-05 |
| gb AF283579.1 AF283579 | Elaphe obsoleta CAS 203079 cytochrom... | 50 | 2e-05 |
| gb AF283578.1 AF283578 | Elaphe obsoleta LSUMZ H2286 cytochro... | 50 | 2e-05 |
| gb AF283577.1 AF283577 | Elaphe obsoleta CAS 208631 cytochrom... | 50 | 2e-05 |
| gb AF283576.1 AF283576 | Elaphe obsoleta LSUMZ H2229 cytochro... | 50 | 2e-05 |
| gb AF187030.1 AF187030 | Rhinophylla pumilio isolate TK46001 ... | 50 | 2e-05 |
| gb AF310052.1 AF310052 | Poospiza hispaniolensis cytochrome b... | 50 | 2e-05 |
| gb AF310046.1 AF310046 | Volatinia jacarina cytochrome b gene... | 50 | 2e-05 |
| gb AF171919.1 AF171919 | Deinagkistrodon acutus cytochrome b ... | 50 | 2e-05 |
| gb AF171897.1 AF171897 | Trimeresurus mucrosquamatus cytb gen... | 50 | 2e-05 |
| gb AF290174.1 AF290174 | Agelaius cyanopus cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF290173.1 AF290173 | Agelaius phoeniceus cytochrome b (cy...) | 50 | 2e-05 |
| gb AF290171.1 AF290171 | Quiscalus major cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF290170.1 AF290170 | Amblycercus holosericeus cytochrome ... | 50 | 2e-05 |
| gb AF290150.1 AF290150 | Volatinia jacarina cytochrome b (cyt...) | 50 | 2e-05 |
| gb AF176252.1 AF176252 | Reithrodontomys zacatecae cytochrome... | 50 | 2e-05 |
| gb AF176251.1 AF176251 | Reithrodontomys zacatecae cytochrome... | 50 | 2e-05 |
| gb AF163907.1 AF163907 | Microtus xanthognathus cytochrome b ... | 50 | 2e-05 |
| gb AF163904.1 AF163904 | Microtus pinetorum cytochrome b gene... | 50 | 2e-05 |
| gb AF163901.1 AF163901 | Microtus ochrogaster cytochrome b ge... | 50 | 2e-05 |
| gb AF163899.1 AF163899 | Microtus miurus cytochrome b gene, c... | 50 | 2e-05 |
| gb AF163891.1 AF163891 | Microtus californicus cytochrome B (...) | 50 | 2e-05 |
| gb AF163890.1 AF163890 | Microtus abbreviatus cytochrome B (c... | 50 | 2e-05 |
| gb AF288524.1 AF288524 | Dipsochelys dussumieri isolate Germa... | 50 | 2e-05 |
| gb AF288523.1 AF288523 | Dipsochelys dussumieri isolate white... | 50 | 2e-05 |
| gb AF288522.1 AF288522 | Dipsochelys dussumieri isolate Aldy ... | 50 | 2e-05 |
| gb AF123530.1 AF123530 | Psilopogon pyrolophus cytochrome b (...) | 50 | 2e-05 |
| gb AF123512.1 AF123512 | Eubucco bourcierii cucinkae cytochro... | 50 | 2e-05 |
| gb AF206548.1 AF206548 | Adolfus vauereselli cytochrome b gen... | 50 | 2e-05 |
| gb AF197867.1 AF197867 | Gymnorhina tibicen cytochrome b gene... | 50 | 2e-05 |
| gb U63397.2 SEU63397 | Sitta europaea cytochrome b gene, part... | 50 | 2e-05 |
| ref NC 001945.1 | Dinodon semicarinatus mitochondrion, compl... | 50 | 2e-05 |
| ref NC 001831.1 | Dasypus novemcinctus mitochondrion, comple... | 50 | 2e-05 |
| gb AF141317.1 AF141317 | Dasymys incomtus country Tanzania cy... | 50 | 2e-05 |
| gb AF201615.1 AF201615 | Pantodon buchholzi cytochrome b gene... | 50 | 2e-05 |
| gb AF077920.1 AF077920 | Bombus nevadensis cytochrome b gene... | 50 | 2e-05 |
| gb AF190612.1 AF190612 | Oreamnos americanus cytochrome b (cy... | 50 | 2e-05 |
| gb J01124.1 BOVMT | Bos taurus mitochondrion, complete genome | 50 | 2e-05 |
| gb AF191810.1 AF191810 | Cochlearius cochlearius cytochrome b... | 50 | 2e-05 |

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| gb U89161.1 CAU89161 | Chlorostilbon aureoventris cytochrome ... | 50 | 2e-05 |
| gb U89171.1 AFU89171 | Asio flammeus cytochrome b (cytb) gene... | 50 | 2e-05 |
| gb AF217811.1 AF217811 | Homoroselaps lacteus cytochrome b ge... | 50 | 2e-05 |
| gb AF217822.1 AF217822 | Hydrophis semperi cytochrome b gene... | 50 | 2e-05 |
| gb AF217813.1 AF217813 | Acanthophis antarcticus cytochrome b... | 50 | 2e-05 |
| gb AF220406.1 AF220406 | Calliophis kelloggi cytochrome b (cy... | 50 | 2e-05 |
| gb AF126430.1 AF126430 | Ellobius fuscocapillus cytochrome b ... | 50 | 2e-05 |
| gb AF090337.1 AF090337 | Aythya americana mitochondrion, comp... | 50 | 2e-05 |
| gb AF059111.1 AF059111 | Sarkidiornis melanotos cytochrome b ... | 50 | 2e-05 |
| gb AF059053.1 AF059053 | Aix sponsa cytochrome b gene, partia... | 50 | 2e-05 |
| gb AF099308.1 AF099308 | Icterus wagleri wagleri cytochrome b... | 50 | 2e-05 |
| gb AF099295.1 AF099295 | Icterus gularis yucatanensis cytochr... | 50 | 2e-05 |
| gb AF099294.1 AF099294 | Icterus gularis tamaulipensis cytoch... | 50 | 2e-05 |
| gb AF099293.1 AF099293 | Icterus gularis gularis cytochrome b... | 50 | 2e-05 |
| gb AF160610.1 AF160610 | Cricetomys emini Cemi636 cytochrome ... | 50 | 2e-05 |
| gb AF036280.1 AF036280 | Tragelaphus strepsiceros cytochrome ... | 50 | 2e-05 |
| gb AF036277.1 AF036277 | Tragelaphus scriptus cytochrome b (c... | 50 | 2e-05 |
| gb AF036274.1 AF036274 | Tetracerus quadricornis cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF194218.1 AF194218 | Phrynosoma platyrhinos cytochrome b ... | 50 | 2e-05 |
| gb AF194216.1 AF194216 | Urosaurus ornatus cytochrome b gene... | 50 | 2e-05 |
| ref NC_002009.1 NC_002009 | Artibeus jamaicensis mitochondrion, comple... | 50 | 2e-05 |
| ref NC_001941.1 NC_001941 | Ovis aries mitochondrion, complete genome | 50 | 2e-05 |
| ref NC_000877.1 NC_000877 | Aythya americana mitochondrion, complete g... | 50 | 2e-05 |
| ref NC_000846.1 NC_000846 | Rhea americana mitochondrion, complete genome | 50 | 2e-05 |
| gb U27551.1 GCU27551 | Grus canadensis tabida cytochrome b (c... | 50 | 2e-05 |
| gb AF089058.1 AF089058 | Quiscalus quiscula cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089055.1 AF089055 | Quiscalus major cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF089054.1 AF089054 | Quiscalus lugubris cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089046.1 AF089046 | Oreopsar bolivianus cytochrome b (cy... | 50 | 2e-05 |
| gb AF089042.1 AF089042 | Molothrus badius cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF089039.1 AF089039 | Macroagelaius imthurni cytochrome b ... | 50 | 2e-05 |
| gb AF089037.1 AF089037 | Lamprospira tanagra cytochrome b (...) | 50 | 2e-05 |
| gb AF089026.1 AF089026 | Gymnomystax mexicanus cytochrome b (...) | 50 | 2e-05 |
| gb AF089025.1 AF089025 | Gnorimopsar chopi cytochrome b (cytb... | 50 | 2e-05 |
| gb AF089024.1 AF089024 | Euphagus cyanocephalus cytochrome b ... | 50 | 2e-05 |
| gb AF089023.1 AF089023 | Euphagus carolinus cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089021.1 AF089021 | Dives wartszewiczi cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089020.1 AF089020 | Curaeus curaeus cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF089016.1 AF089016 | Amblycercus holosericeus cytochrome ... | 50 | 2e-05 |
| gb AF089013.1 AF089013 | Agelaius xanthophthalmus cytochrome ... | 50 | 2e-05 |
| gb AF089012.1 AF089012 | Agelaius xanthomus cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089008.1 AF089008 | Agelaius phoeniceus sub-species phoe... | 50 | 2e-05 |
| gb AF089006.1 AF089006 | Agelaius humeralis cytochrome b (cyt... | 50 | 2e-05 |
| gb AF089005.1 AF089005 | Agelaius cyanopus cytochrome b (cytb... | 50 | 2e-05 |
| gb AF108696.1 AF108696 | Scolomys juruaense cytochrome B (cyt... | 50 | 2e-05 |
| gb AF108685.1 AF108685 | Wiedomys pyrrhorhinos cytochrome B (...) | 50 | 2e-05 |
| gb AF108677.1 AF108677 | Thomasomys oreas cytochrome B (cytB)... | 50 | 2e-05 |
| gb AF145511.1 AF145511 | Melanoplus foedus cytochrome b gene... | 50 | 2e-05 |
| gb AF145511.1 AF145511 | Melanoplus angustipennis cytochrome ... | 50 | 2e-05 |
| gb U89627.1 BMU89627 | Bolitoglossa macrinosa cytochrome b (cy... | 50 | 2e-05 |
| gb U89623.1 BPU89623 | Batrachoseps pacificus cytochrome b (c... | 50 | 2e-05 |
| gb AF181470.1 AF181470 | Okapia johnstoni cytochrome b gene... | 50 | 2e-05 |
| gb AF084075.1 AF084075 | Lagenorhynchus acutus cytochrome b g... | 50 | 2e-05 |
| gb U90303.1 OMU90303 | Ovibos moschatus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U90302.1 OMU90302 | Ovibos moschatus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U90301.1 OMU90301 | Ovibos moschatus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U90300.1 OMU90300 | Ovibos moschatus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb AF038883.1 AF038883 | Deinagkistrodon acutus cytochrome b ... | 50 | 2e-05 |
| gb AF039268.1 AF039268 | Agkistrodon contortrix cytochrome b ... | 50 | 2e-05 |
| gb AF039267.1 AF039267 | Boa constrictor cytochrome b (cytb) ... | 50 | 2e-05 |
| gb S49215.1 S49215 | apocytochrome b (sheep, domestic, Merino... | 50 | 2e-05 |
| gb AF158698.1 AF158698 | Geomys pinetis cytochrome b gene, co... | 50 | 2e-05 |
| gb AF158692.1 AF158692 | Geomys bursarius jugoslavicus cyto... | 50 | 2e-05 |
| gb AF058193.1 AF058193 | Ichaginia cruentus cytochrome b (cyt... | 50 | 2e-05 |
| gb AF091629.1 AF091629 | Ancilocapra americana cytochrome b (...) | 50 | 2e-05 |
| gb AF022062.1 AF022062 | Tragelaphus strepsiceros cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF022062.1 AF022062 | Tragelaphus decbianus cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb AF022060.1 AF022060 | Hippotragus equinus cytochrome b (cytb) gene... | 50 | 2e-05 |
| gb AF022057.1 AF022057 | Tragelaphus oryx cytochrome b (cytb) gene, m... | 50 | 2e-05 |
| gb AF111500.1 AF111500 | Lagenorhynchus acutus isolate LACU74... | 50 | 2e-05 |
| gb AF111499.1 AF111499 | Lagenorhynchus acutus isolate LACU75... | 50 | 2e-05 |

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| gb U69740.1 ESU69740 | Lexocemus bicolor cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Eunectes notaeus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Eunectes murinus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates striatus fosteri cytochrome... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates striatus strigilatus cytochr... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates striatus strigilatus cytochr... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates striatus mceraniei cytochrom... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates striatus mceraniei cytochrom... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates monensis cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates monensis cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates fordii cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates fordii cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates cenchria cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates cenchria cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates angulifer cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Epicrates angulifer cytochrome b (cytb)... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Corallus enydris cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Corallus enydris cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Corallus enydris cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Corallus enydris cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Corallus enydris cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Candoia aspera cytochrome b (cytb) gen... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Boa constrictor cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U69740.1 ESU69740 | Boa constrictor cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb AF139057.1 AF139057 | Isoodon macrourus cytochrome b gene,... | 50 | 2e-05 |
| gb AF090339.1 AF090339 | Rhea americana mitochondrion, comple... | 50 | 2e-05 |
| gb AF006275.1 AF006275 | Cnemidophorus tigris strain Isla Ang... | 50 | 2e-05 |
| gb AF006275.1 AF006275 | Cnemidophorus tigris strain Isla Smi... | 50 | 2e-05 |
| gb AF006275.1 AF006275 | Connochaetes taurinus cytochrome b g... | 50 | 2e-05 |
| gb AF028822.1 AF028822 | Alcelaphus buselaphus cytochrome b g... | 50 | 2e-05 |
| gb AF028822.1 AF028822 | Damaliscus lunatus cytochrome b gene... | 50 | 2e-05 |
| gb AF061340.1 AF061340 | Artibeus jamaicensis mitochondrial D... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Thalassarche impavida cytochrome b (...) | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Thalassarche carteri cytochrome b (c... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Pelagodroma marina cytochrome b (cyt... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Oceanodroma furcata cytochrome b (cy... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Hydrobates pelagicus cytochrome b (c... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Garrodia nereis cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Fregetta tropica cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Diomedea gibsoni cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Diomedea epomophora cytochrome b (cy... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Diomedea chionopectera cytochrome b (c... | 50 | 2e-05 |
| gb AF076093.1 AF076093 | Diomedea antipodensis cytochrome b (...) | 50 | 2e-05 |
| gb U83314.1 MSU83314 | Microhierax semitorquatus cytochrome b (...) | 50 | 2e-05 |
| gb U83314.1 MSU83314 | Microhierax erythrogenys cytochrome b ... | 50 | 2e-05 |
| gb U37303.1 SAU37303 | Synthliboramphus antiquus cytochrome b... | 50 | 2e-05 |
| gb U37303.1 SAU37303 | Ptychoramphus aleuticus cytochrome b g... | 50 | 2e-05 |
| gb U37296.1 CPU37296 | Cyclorhynchus psittacula cytochrome b... | 50 | 2e-05 |
| gb U37296.1 CPU37296 | Brachyramphus brevirostris cytochrome ... | 50 | 2e-05 |
| gb U37296.1 CPU37296 | Aethia pygmaea cytochrome b gene, mito... | 50 | 2e-05 |
| gb U37296.1 CPU37296 | Aethia pusilla cytochrome b gene, mito... | 50 | 2e-05 |
| gb U37087.1 ACU37087 | Aethia cristatella cytochrome b gene, ... | 50 | 2e-05 |
| gb U87524.1 HGU87524 | Heterocephalus glaber cytochrome-b gen... | 50 | 2e-05 |
| gb U87524.1 HGU87524 | Heterocephalus glaber cytochrome-b gen... | 50 | 2e-05 |
| gb U87524.1 HGU87524 | Heterocephalus glaber cytochrome-b gen... | 50 | 2e-05 |
| gb U87524.1 HGU87524 | Heterocephalus glaber cytochrome-b gen... | 50 | 2e-05 |
| gb U17864.1 STU17864 | Saiga tatarica cytochrome b gene, mito... | 50 | 2e-05 |
| gb U17864.1 STU17864 | Oreamnos americanus cytochrome b gene... | 50 | 2e-05 |
| gb U17864.1 STU17864 | Ovibos moschatus moschatus cytochrome ... | 50 | 2e-05 |
| gb U17864.1 STU17864 | Ovis dalli cytochrome b gene, mitochon... | 50 | 2e-05 |
| gb U17864.1 STU17864 | Ovis canadensis cytochrome b gene, mit... | 50 | 2e-05 |
| gb U65274.1 TBU65274 | Thomomys bottae cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U65274.1 TBU65274 | Thomomys bottae cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U65274.1 TBU65274 | Thomomys bottae cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U65274.1 TBU65274 | Thomomys bottae cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U65274.1 TBU65274 | Perognathus amplius cytochrome b (cytb)... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Capra aegagrus cytochrome b (cytb) g... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Capra caucasica cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Capra cylindricornis cytochrome b (cytb) gen... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Capra falconeri cytochrome b (cytb) ... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Capra ibex cytochrome b (cytb) gene, mitoch... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Ovis aries cytochrome b (cytb) gene... | 50 | 2e-05 |
| gb AF034739.1 AF034739 | Ovis vignei cytochrome b (cytb) gene... | 50 | 2e-05 |

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| gb AF034724.1 | Ovis dalli dalli cytochrome b (cytb) gene. m... | 50 | 2e-05 |
| gb AF034727.1 | Ovis ammon darwini cytochrome b (cytb) gene. | 50 | 2e-05 |
| gb AF034724.1 AF034724 | Pantholops hodgsoni cytochrome b (cy... | 50 | 2e-05 |
| gb AF057132.1 AF057132 | Taxidea taxus cytochrome b (cytb) ge... | 50 | 2e-05 |
| gb U54805.1 TMU94805 | Trogon melanurus cytochrome b gene, mi... | 50 | 2e-05 |
| gb U54804.1 TCU94804 | Trogon comptus cytochrome b gene, mito... | 50 | 2e-05 |
| gb U94803.1 TVU94803 | Trogon viridis cytochrome b gene, mito... | 50 | 2e-05 |
| gb AF006232.1 AF006231 | Sericossypha albocristata cytochrome... | 50 | 2e-05 |
| gb AF006249.1 AF006249 | Pyrrhocoma ruficeps cytochrome b (cy... | 50 | 2e-05 |
| gb AF006238.1 AF006238 | Lamprospiza melanoleuca cytochrome b... | 50 | 2e-05 |
| gb AF006234.1 AF006234 | Hemispingus atropileus cytochrome b ... | 50 | 2e-05 |
| gb AF005226.1 AF006226 | Cypsnagra hirundinacea cytochrome b ... | 50 | 2e-05 |
| gb AF006215.1 AF006215 | Chlorophanes spiza cytochrome b (cyt... | 50 | 2e-05 |
| gb AF006214.1 AF006214 | Chlorochrysa calliparaea cytochrome ... | 50 | 2e-05 |
| gb AF006213.1 AF006213 | Calochaetes coccineus cytochrome b (...) | 50 | 2e-05 |
| gb AF006212.1 AF006212 | Buchraupis montana cytochrome b (cyt... | 50 | 2e-05 |
| emb AJ293419.1 RRU293419 | Rupicapra rupicapra rupicapra mito... | 50 | 2e-05 |
| emb AJ293416.1 RPY293416 | Rupicapra pyrenaica pyrenaica mito... | 50 | 2e-05 |
| emb AJ293415.1 RPY293415 | Rupicapra pyrenaica parva mitochon... | 50 | 2e-05 |
| emb AJ293414.1 RPY293414 | Rupicapra pyrenaica ornata mitochon... | 50 | 2e-05 |
| emb AJ293412.1 RRU293412 | Rupicapra rupicapra rupicapra mito... | 50 | 2e-05 |
| emb AJ293418.1 CFA293418 | Capra falconeri mitochondrial part... | 50 | 2e-05 |
| gb U07578.1 DCU07578 | Dasycercus cristicauda mitochondrial c... | 50 | 2e-05 |
| emb AJ004180.1 HPAJ4180 | Hydrobates pelagicus mitochondrial ... | 50 | 2e-05 |
| emb Y15695.1 SMY15695 | Schilbe mystus mitochondrial cytb gen... | 50 | 2e-05 |
| emb Y15697.1 EDY15697 | Eutropius depressirostris mitochondri... | 50 | 2e-05 |
| emb Y15696.1 EDY15696 | Eutropius depressirostris mitochondri... | 50 | 2e-05 |
| gb AF015035.1 AF015035 | Steatocranus casuarinus 20 cytochrom... | 50 | 2e-05 |
| gb AF015761.1 AF015761 | Palmeria dolei cytochrome b (Cytb) g... | 50 | 2e-05 |
| gb AF015758.1 AF015758 | Oreomystis mana cytochrome b (Cytb) ... | 50 | 2e-05 |
| gb AF015756.1 AF015756 | Vestiaria coccinea cytochrome b (Cyt... | 50 | 2e-05 |
| gb AF015754.1 AF015754 | Himatione sanguinea cytochrome b (Cy... | 50 | 2e-05 |
| gb U76052.1 DMU76052 | Dromaius novaehollandiae cytochrome b ... | 50 | 2e-05 |
| emb AJ236834.1 CGU236834 | Clethrionomys glareolus mitochondr... | 50 | 2e-05 |
| gb U83158.1 POU83158 | Pelecanus onocrotalus cytochrome B gen... | 50 | 2e-05 |
| gb U83157.1 POU83157 | Pelecanus onocrotalus cytochrome B gen... | 50 | 2e-05 |
| gb U83156.1 AAU83156 | Anhinga anhinga cytochrome B gene, mit... | 50 | 2e-05 |
| gb U83155.1 AAU83155 | Anhinga anhinga cytochrome B gene, mit... | 50 | 2e-05 |
| gb U83154.1 AAU83154 | Anhinga anhinga cytochrome B gene, mit... | 50 | 2e-05 |
| gb U83156.1 CLU83156 | Chelodina longicollis cytochrome b gen... | 50 | 2e-05 |
| emb AJ277676.1 ESC277676 | Elaphe scalaris mitochondrial part... | 50 | 2e-05 |
| emb AJ277675.1 ESC277675 | Elaphe scalaris mitochondrial part... | 50 | 2e-05 |
| emb AJ277672.1 ELO277672 | Elaphe longissima mitochondrial pa... | 50 | 2e-05 |
| emb AJ277671.1 ELO277671 | Elaphe longissima mitochondrial pa... | 50 | 2e-05 |
| emb Y11832.1 MTNCOMGN | Dasypus novemcinctus complete mitoch... | 50 | 2e-05 |
| emb AJ388467.1 NBA388467 | Nemacheilus barbatulus mitochondria... | 50 | 2e-05 |
| emb AJ388468.1 IME388468 | Ictalurus melas mitochondrial cyt b... | 50 | 2e-05 |
| emb AJ388459.1 LDE388459 | Leucaspius delineatus mitochondrial... | 50 | 2e-05 |
| gb U46167.1 SCU46167 | Sciurus carolinensis cytochrome b gene... | 50 | 2e-05 |
| emb AJ245673.1 SIN245673 | Schilbe intermedius partial mitoch... | 50 | 2e-05 |
| emb AJ245638.1 SIN245638 | Schilbe intermedius partial mitoch... | 50 | 2e-05 |
| emb AJ245678.1 EDE245678 | Eutropius depressirostris partial ... | 50 | 2e-05 |
| emb AJ245677.1 EDE245677 | Eutropius depressirostris partial ... | 50 | 2e-05 |
| emb AJ245676.1 EDE245676 | Eutropius depressirostris partial ... | 50 | 2e-05 |
| emb AJ245675.1 EDE245675 | Eutropius depressirostris partial ... | 50 | 2e-05 |
| emb AJ245674.1 EDE245674 | Eutropius depressirostris partial ... | 50 | 2e-05 |
| emb Y15884.3 MTRACOMPL | Rhea americana complete mitochondria... | 50 | 2e-05 |
| gb U60768.1 PCU60768 | Parus cinctus cytochrome b gene, mitoc... | 50 | 2e-05 |
| gb U48955.1 TMU48955 | Thalassarche melanophris melanophris c... | 50 | 2e-05 |
| gb U48954.1 TCU48954 | Thalassarche chrysostoma cytochrome b ... | 50 | 2e-05 |
| gb U48944.1 TCU48944 | Thalassarche chlororhynchus chlororhyn... | 50 | 2e-05 |
| gb U48943.1 PPU48943 | Phoebastria palpebrata cytochrome b (cy... | 50 | 2e-05 |
| gb U48942.1 PFU48942 | Phoebastria fusca cytochrome b (cytb) g... | 50 | 2e-05 |
| gb U48941.1 MCU48941 | Macronectes giganteus cytochrome b (cy... | 50 | 2e-05 |
| gb U48947.1 DEU48947 | Diomedea exulans dabbenena cytochrome ... | 50 | 2e-05 |
| gb U48946.1 DEU48946 | Diomedea epomophora sanfordi cytochrom... | 50 | 2e-05 |
| gb U48949.1 DAU48949 | Diomedea amsterdamensis cytochrome b (...) | 50 | 2e-05 |
| gb U55525.1 PRU55525 | Piranga rubra cytochrome b gene, mitoc... | 50 | 2e-05 |
| gb U55509.1 APU55509 | Artibeus planirostris cytochrome b (cy... | 50 | 2e-05 |
| gb U55507.1 AQU55507 | Artibeus obscurus cytochrome b (cytb) ... | 50 | 2e-05 |
| gb U55506.1 AQU55506 | Artibeus obscurus cytochrome b (cytb) ... | 50 | 2e-05 |

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|--------------------------|--|----|-------|
| gb U66505.1 ALUG6505 | Artibeus lituratus cytochrome b (cytb)... | 50 | 2e-05 |
| gb U66504.1 AJUG6504 | Artibeus jamaicensis cytochrome b (cyt... | 50 | 2e-05 |
| gb U66503.1 AJUG6503 | Artibeus jamaicensis cytochrome b (cyt... | 50 | 2e-05 |
| gb U66502.1 AIUG6502 | Artibeus intermedius cytochrome b (cyt... | 50 | 2e-05 |
| gb U66501.1 AU66501 | Artibeus inopinatus cytochrome b (cytb... | 50 | 2e-05 |
| gb U66500.1 AHU66500 | Artibeus hirsutus cytochrome b (cytb)... | 50 | 2e-05 |
| gb U66499.1 AFU66499 | Artibeus fraterculus cytochrome b (cyt... | 50 | 2e-05 |
| gb U66498.1 AFU66499 | Artibeus fimbriatus cytochrome b (cytb... | 50 | 2e-05 |
| gb U63061.1 BBU63061 | Brachyramphus brevirostris cytochrome... | 50 | 2e-05 |
| gb U63060.1 BBU63060 | Brachyramphus brevirostris cytochrome... | 50 | 2e-05 |
| gb U63059.1 BBU63059 | Brachyramphus brevirostris cytochrome... | 50 | 2e-05 |
| gb U63058.1 BBU63058 | Brachyramphus brevirostris cytochrome... | 50 | 2e-05 |
| gb U58386.1 SJU58386 | Scolomys juruaense cytochrome b (cyt-b... | 50 | 2e-05 |
| gb L11905.1 CGYMTCTYBD | Cratogeomys gymnotus mitochondrial c... | 50 | 2e-05 |
| gb U34672.1 MNU34672 | Metachirus nudicaudatus cytochrome b l... | 50 | 2e-05 |
| gb U34671.1 MNU34671 | Metachirus nudicaudatus cytochrome b l... | 50 | 2e-05 |
| emb Y14951.1 MTY14951 | Capreolus capreolus mitochondrial cyt... | 50 | 2e-05 |
| emb Y14371.1 MTCCCYTB | Capreolus capreolus mitochondrial cyt... | 50 | 2e-05 |
| gb L11909.1 CGYMTCTYBH | Cratogeomys tylosinus mitochondrial... | 50 | 2e-05 |
| gb L11901.1 PPGMYCTYBB | Geomys bursarius jugosicircularis mito... | 50 | 2e-05 |
| gb L11904.1 CGYMTCTYBC | Cratogeomys goldmani goldmani mitoch... | 50 | 2e-05 |
| emb X94928.1 SPCYTB | S. putorius mitochondrial DNA for cytoch... | 50 | 2e-05 |
| gb U46770.1 ARU46770 | Anthus richardi cytochrome b gene, mit... | 50 | 2e-05 |
| gb U46769.1 ABU46769 | Anthus berthelotii cytochrome b gene, ... | 50 | 2e-05 |
| gb U46183.1 SSU46183 | Sciurus sciramineus cytochrome b gene, ... | 50 | 2e-05 |
| emb Y10728.1 PSMY10728 | P. schwarzi mitochondrial cytb gene, ... | 50 | 2e-05 |
| emb X95768.1 NLMCB | N. leucopterus mitochondrial cytochrome b... | 50 | 2e-05 |
| emb X95767.1 NGRIMCB | N. griseus mitochondrial cytochrome b gene | 50 | 2e-05 |
| emb X86763.1 MTVGCYT26 | V. gryphus mitochondrial cytb gene | 50 | 2e-05 |
| emb X86754.1 MTLCCYT17 | L. crumeniferus mitochondrial cytb gene | 50 | 2e-05 |
| emb X86743.1 MTCACYT6 | C. aura mitochondrial cytb gene | 50 | 2e-05 |
| dbj AB035242.1 AB035242 | Pantodon buchholzi mitochondrial cy... | 50 | 2e-05 |
| emb X60946.1 MITDC333 | T. dorbignyi mitochondrial gene for c... | 50 | 2e-05 |
| emb AJ000029.1 MIRTCYB29 | Rangifer tarandus mitochondrial cy... | 50 | 2e-05 |
| emb X82302.1 MIPFCYTBG | P. fasciata mitochondrial cytochrome... | 50 | 2e-05 |
| emb X56291.1 MIOHCYTB | O. hemionus mitochondrion cytb gene fo... | 50 | 2e-05 |
| emb X56284.1 MIOACYTB | O. aries mitochondrion cytb gene for c... | 50 | 2e-05 |
| emb AJ000022.1 MIMSCYB22 | Dama dama mitochondrial cytb gene | 50 | 2e-05 |
| emb X72005.1 MILWCYTB | L. weddelli mitochondrial gene for cyt... | 50 | 2e-05 |
| emb Y08814.1 MIHLCYTBG | H. liberiensis mitochondrial cytochro... | 50 | 2e-05 |
| emb X60942.1 MIGTC311 | Gymnorhina tibicen mitochondrial gene... | 50 | 2e-05 |
| emb X56290.1 MIDDCYTB | D. dama mitochondrion cytb gene for cy... | 50 | 2e-05 |
| emb AJ000021.1 MICECYB21 | Cervus elaphus mitochondrial cytb... | 50 | 2e-05 |
| emb AJ000024.1 MICCCYB24 | Capreolus capreolus mitochondrial... | 50 | 2e-05 |
| emb V00654.1 MI3TXX | Bos taurus complete mitochondrial genome | 50 | 2e-05 |
| emb X56286.1 MIAACYTB | A. americana mitochondrion cytb gene... | 50 | 2e-05 |
| gb L19718.1 AJUMTCYTB | Artibeus lituratus mitochondrial cyto... | 50 | 2e-05 |
| gb U27543.1 BRU27543 | Balearica regulorum cytochrome b (cytb... | 50 | 2e-05 |
| dbj AB030025.1 AB030025 | Sciurus sciramineus mitochondrial cy... | 50 | 2e-05 |
| gb U18258.1 SCU18258 | Spharagemon campestris cytochrome b ge... | 50 | 2e-05 |
| gb U18257.1 SCU18257 | Spharagemon collare cytochrome b gene... | 50 | 2e-05 |
| gb U18253.1 TPU18253 | Trimerotropis pistrinaria cytochrome b... | 50 | 2e-05 |
| gb U18250.1 CPU18250 | Camnula pallucida cytochrome b gene, m... | 50 | 2e-05 |
| gb U17904.1 CCU17904 | Circotettix carlinianus mitochondrion... | 50 | 2e-05 |
| dbj D84202.1 GOTMTCB8 | Capra falconeri mitochondrial DNA for... | 50 | 2e-05 |
| dbj D82889.1 D82889 | Bos javanicus mitochondrial DNA for cyt... | 50 | 2e-05 |
| dbj D32195.1 CCRMTCB25 | Capricornis sumatrensis mitochondrial... | 50 | 2e-05 |
| dbj D32191.1 CCRMTCB21 | Capricornis crispus mitochondrial ge... | 50 | 2e-05 |
| dbj AB021098.1 AB021098 | Cervus elaphus kansuensis mitochond... | 50 | 2e-05 |
| dbj AB021097.1 AB021097 | Cervus elaphus xanthopygus mitochon... | 50 | 2e-05 |
| dbj AB021095.1 AB021095 | Cervus nippon yezoensis mitochondri... | 50 | 2e-05 |
| dbj AB021094.1 AB021094 | Cervus nippon centralis mitochondri... | 50 | 2e-05 |
| dbj AB021092.1 AB021092 | Cervus nippon mageshimae mitochondr... | 50 | 2e-05 |
| dbj AB021091.1 AB021091 | Cervus nippon keramae mitochondrial... | 50 | 2e-05 |
| dbj AB001612.1 AB001612 | Cervus elaphus mitochondrial DNA fo... | 50 | 2e-05 |
| dbj D84205.1 SHPMTCB6 | Sheep mitochondrial DNA for cytochrom... | 50 | 2e-05 |
| dbj D84203.1 SHPMTCB3 | Ovis musimon mitochondrial DNA for cy... | 50 | 2e-05 |
| dbj D74456.1 BOVMTCB8 | Bos javanicus mitochondrial gene for... | 50 | 2e-05 |
| dbj D74455.1 BOVMTCB | Bovine mitochondrial gene for cytochr... | 50 | 2e-05 |
| dbj D72178.1 ORMTCB28 | Oreamnos americanus mitochondrial ge... | 50 | 2e-05 |
| dbj D72175.1 NAGMTCB26 | Nemorhaedus goral mitochondrial gene... | 50 | 2e-05 |

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| dbj D32182.1 CEUMTCB11 | Cervus nippon mitochondrial gene for... | 50 | 2e-05 |
| dbj AB021094.1 AB021094 | Cervus elaphus scoticus mitochondri... | 50 | 2e-05 |
| dbj AB021096.1 AB021096 | Cervus elaphus canadensis mitochond... | 50 | 2e-05 |
| dbj AB021093.1 AB021093 | Cervus nippon nippon mitochondrial ... | 50 | 2e-05 |
| dbj AB021090.1 AB021090 | Cervus nippon pulchellus mitochondr... | 50 | 2e-05 |
| dbj AB006539.1 AB006539 | Dinodon semicarinatus mitochondrial... | 50 | 2e-05 |
| dbj AB006800.1 AB006800 | Ovis aries mitochondrial DNA for cy... | 50 | 2e-05 |
| gb L12763.1 LDHMTCTB | Lepidochelys kempi (LK-3) mitochondri... | 50 | 2e-05 |
| gb L08032.1 CPLMTCYTA | Carcharhinus plumbeus mitochondrial ... | 50 | 2e-05 |
| gb L28941.1 URRCYS | Uroderma bilobatum cytochrome b gene, 5'... | 50 | 2e-05 |
| gb L28937.1 CDECYB | Chiroderma doriae cytochrome b gene, 5' end | 50 | 2e-05 |
| emb AJ010056.1 CPY010056 | Capra pyrenaica (individual 12) mi... | 50 | 2e-05 |
| emb AJ010054.1 CPY010054 | Capra pyrenaica (individual 11) mi... | 50 | 2e-05 |
| emb AJ010053.1 CPY010053 | Capra pyrenaica (individual 10) mi... | 50 | 2e-05 |
| emb AJ010052.1 CPY010052 | Capra pyrenaica (individual 9) mit... | 50 | 2e-05 |
| emb AJ010051.1 CPY010051 | Capra pyrenaica (individual 8) mit... | 50 | 2e-05 |
| emb AJ010050.1 CPY010050 | Capra pyrenaica (individual 7) mit... | 50 | 2e-05 |
| emb AJ010049.1 CPY010049 | Capra pyrenaica (individual 6) mit... | 50 | 2e-05 |
| emb AJ010048.1 CPY010048 | Capra pyrenaica (individual 5) mit... | 50 | 2e-05 |
| emb AJ010047.1 CPY010047 | Capra pyrenaica (individual 4) mit... | 50 | 2e-05 |
| emb X95777.1 CLMCB | C. longirostris mitochondrial cytochrome ... | 50 | 2e-05 |
| emb AJ009879.1 CIB9879 | Capra ibex nubiana mitochondrial cyt... | 50 | 2e-05 |
| emb AJ010055.1 CIB010055 | Capra ibex (individual 1) ibex mit... | 50 | 2e-05 |
| gb U08946.1 CAU08946 | Coragyps atratus mitochondrion cytochr... | 50 | 2e-05 |
| gb U08945.1 CBU08945 | Cathartes burrovianus mitochondrion cy... | 50 | 2e-05 |
| gb U08944.1 VGU08944 | Vultur gryphus mitochondrion cytochrom... | 50 | 2e-05 |
| gb U08941.1 PAU08941 | Platalea alba mitochondrion cytochrome... | 50 | 2e-05 |
| gb U08940.1 PRU08940 | Phoenicopterus ruber mitochondrion cyt... | 50 | 2e-05 |
| emb X95775.1 ACMCB | A. cristatus mitochondrial cytochrome b gene | 50 | 2e-05 |
| emb X95774.1 ABMCB | A. bennettii mitochondrial cytochrome b gene | 50 | 2e-05 |
| emb X95764.1 AAMCB | A. albertisi mitochondrial cytochrome b gene | 43 | 8e-05 |
| gb AF040383.1 AF040383 | Alces alces cytochrome b (cytb) gene... | 46 | 3e-04 |
| gb AF232023.1 AF232023 | Tamandua tetradactyla clone 7 cytoch... | 46 | 3e-04 |
| gb AF232022.1 AF232022 | Tamandua tetradactyla clone 6 mitoch... | 46 | 3e-04 |
| gb AF232021.1 AF232021 | Tamandua tetradactyla clone 5 cytoch... | 46 | 3e-04 |
| gb AF157466.1 AF157466 | Lepus timidus cytochrome b (Cyb) gen... | 46 | 3e-04 |
| gb AF157465.1 AF157465 | Lepus granatensis cytochrome b (Cyb)... | 46 | 3e-04 |
| gb AF157464.1 AF157464 | Lepus corsicanus haplotype 1 cytochr... | 46 | 3e-04 |
| gb AF157463.1 AF157463 | Lepus corsicanus haplotype 3 cytochr... | 46 | 3e-04 |
| gb AF157460.1 AF157460 | Lepus europaeus cytochrome b (Cyb) g... | 46 | 3e-04 |
| gb AF231664.1 AF231664 | Tylosurus crocodilus crocodilus cyto... | 46 | 3e-04 |
| gb AF231663.1 AF231663 | Tylosurus crocodilus clone STR1-1937... | 46 | 3e-04 |
| gb AF231662.1 AF231662 | Tylosurus crocodilus clone HB-156 cy... | 46 | 3e-04 |
| gb AF231660.1 AF231660 | Tylosurus acus pacificus cytochrome ... | 46 | 3e-04 |
| gb AF231659.1 AF231659 | Tylosurus acus melanotus clone STR1... | 46 | 3e-04 |
| gb AF231658.1 AF231658 | Tylosurus acus melanotus clone STR1... | 46 | 3e-04 |
| gb AF231657.1 AF231657 | Tylosurus acus imperialis cytochrome... | 46 | 3e-04 |
| gb AF231656.1 AF231656 | Tylosurus acus acus cytochrome b oxi... | 46 | 3e-04 |
| gb AF231644.1 AF231644 | Strongylura hubbsi cytochrome b oxid... | 46 | 3e-04 |
| gb AF231639.1 AF231639 | Ablennes hians cytochrome b oxidase ... | 46 | 3e-04 |
| gb AF232019.1 AF232019 | Tamandua tetradactyla clone 3 cytoch... | 46 | 3e-04 |
| gb AF232017.1 AF232017 | Tamandua tetradactyla clone 1 cytoch... | 46 | 3e-04 |
| gb AF232014.1 AF232014 | Myiodon darwini cytochrome b gene... | 46 | 3e-04 |
| gb AF118564.1 AF118564 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118563.1 AF118563 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118562.1 AF118562 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118561.1 AF118561 | Alligator mississippiensis isolate G... | 46 | 3e-04 |
| gb AF118560.1 AF118560 | Alligator mississippiensis isolate G... | 46 | 3e-04 |
| gb AF118559.1 AF118559 | Alligator mississippiensis isolate A... | 46 | 3e-04 |
| gb AF118558.1 AF118558 | Alligator mississippiensis isolate A... | 46 | 3e-04 |
| gb AF118557.1 AF118557 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118556.1 AF118556 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118555.1 AF118555 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118554.1 AF118554 | Alligator mississippiensis isolate S... | 46 | 3e-04 |
| gb AF118553.1 AF118553 | Alligator mississippiensis isolate L... | 46 | 3e-04 |
| gb AF118551.1 AF118551 | Alligator mississippiensis isolate L... | 46 | 3e-04 |
| gb AF118550.1 AF118550 | Alligator mississippiensis isolate F... | 46 | 3e-04 |
| gb AF118549.1 AF118549 | Alligator mississippiensis isolate F... | 46 | 3e-04 |
| gb AF118548.1 AF118548 | Alligator mississippiensis isolate F... | 46 | 3e-04 |
| gb AF118547.1 AF118547 | Sorex monticolus specimen-voucher AF... | 46 | 3e-04 |

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|-------------------------|---|----|-------|
| gb AF126272.1 AF126272 | Myospalax myospalax cytochrome b (cy... | 46 | 3e-04 |
| gb AF126271.1 AF126271 | Myospalax psilurus isolate 2 cytochr... | 46 | 3e-04 |
| gb AF126270.1 AF126270 | Myospalax psilurus isolate 1 cytochr... | 46 | 3e-04 |
| gb AF126266.1 AF126266 | Eospalax fontanierii isolate 4 cytoc... | 46 | 3e-04 |
| emb AJ004340.1 ADAJ4340 | Acrocephalus dumetorum mitochondria... | 44 | 0.001 |
| emb AJ004264.1 ADAJ4264 | Acrocephalus dumetorum mitochondria... | 44 | 0.001 |

Alignments

| | | | |
|-----------|-------|----------------------------|-------|
| cmpseq_0 | 1 | taccatgaggacaaatattcattctg | 25 |
| AF231651 | 398 | | 422 |
| AF231650 | 398 | | 422 |
| NC_002672 | 15560 | | 15584 |
| NC_002673 | 15552 | | 15576 |
| AF232015 | 398 | | 422 |
| AF232013 | 398 | | 422 |
| AY016015 | 15552 | | 15576 |
| AY016013 | 15560 | | 15584 |
| AY016014 | 11516 | | 11540 |
| AF230167 | 266 | | 290 |
| AF074594 | 206 | | 230 |
| AY005210 | 290 | | 314 |
| AY005209 | 290 | | 314 |
| AY005208 | 290 | | 314 |
| AY005205 | 290 | | 314 |
| AY005204 | 290 | | 314 |
| AY005203 | 290 | | 314 |
| AY005201 | 290 | | 314 |
| AY005199 | 290 | | 314 |
| AY005198 | 290 | | 314 |
| AF155870 | 398 | | 422 |
| AF189123 | 326 | | 350 |
| AF102099 | 215 | | 239 |
| AF102095 | 208 | | 232 |
| AF271065 | 398 | | 422 |
| AF243857 | 275 | | 299 |
| AF243856 | 275 | | 299 |
| NC_001567 | 14911 | | 14935 |
| AF306872 | 302 | | 326 |
| AF306871 | 302 | | 326 |
| AF306870 | 302 | | 326 |
| AF306869 | 302 | | 326 |
| AF306868 | 302 | | 326 |
| AF010406 | 14556 | | 14580 |
| AF248662 | 303 | | 327 |
| AF248661 | 303 | | 327 |
| AF096462 | 264 | | 288 |
| AF283644 | 374 | | 398 |
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| AF283635 | 374 | | 398 |
| AF283634 | 374 | | 398 |
| AF283633 | 374 | | 398 |
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| AF283631 | 374 | | 398 |
| AF283630 | 374 | | 398 |
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| AF283628 | 374 | | 398 |
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| AF283620 | 374 | | 398 |

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| <u>AF283619</u> | 374 | | 398 |
| <u>AF283618</u> | 374 | | 398 |
| <u>AF283617</u> | 374 | | 398 |
| <u>AF283616</u> | 374 | | 398 |
| <u>AF283615</u> | 374 | | 398 |
| <u>AF283614</u> | 374 | | 398 |
| <u>AF283613</u> | 374 | | 398 |
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| <u>AF283608</u> | 374 | | 398 |
| <u>AF283607</u> | 374 | | 398 |
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| <u>AF283605</u> | 374 | | 398 |
| <u>AF283604</u> | 374 | | 398 |
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| AF145511 | 169 | | 193 |
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| AF158693 | 398 | | 422 |
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| <u>U17296</u> | 303 | | 327 |
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| <u>U17286</u> | 303 | | 327 |
| <u>U17104</u> | 303 | | 327 |
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| <u>U17859</u> | 329 | | 353 |
| <u>U65274</u> | 398 | | 422 |
| <u>U65267</u> | 398 | | 422 |
| <u>U65260</u> | 398 | | 422 |
| <u>U65191</u> | 398 | | 422 |

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| <u>AF034724</u> | 398 | | 422 |
| <u>AF057132</u> | 396 | | 422 |
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| <u>AJ293415</u> | 398 | | 422 |
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| <u>Y15697</u> | 432 | | 456 |
| <u>Y15696</u> | 432 | | 456 |
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| <u>U83154</u> | 300 | | 324 |
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| <u>AJ388459</u> | 305 | | 329 |
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| <u>U66499</u> | 398 | | 422 |
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| <u>U63061</u> | 302 | | 326 |
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| <u>U63058</u> | 302 | | 326 |
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| <u>Y14371</u> | 398 | | 422 |
| <u>L11909</u> | 398 | | 422 |
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| <u>X86763</u> | 299 | | 323 |
| <u>X86754</u> | 299 | | 323 |
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| <u>D12191</u> | 398 | | 422 |
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| <u>AB021025</u> | 398 | | 422 |
| <u>AB021024</u> | 398 | | 422 |
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| <u>D32192</u> | 398 | | 422 |
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| <u>AB021096</u> | 398 | | 422 |
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| <u>AB021090</u> | 398 | | 422 |
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| <u>AJ010048</u> | 269 | | 293 |
| <u>AJ010047</u> | 269 | | 293 |
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| <u>U08945</u> | 303 | | 327 |
| <u>U08944</u> | 303 | | 327 |
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| <u>U08940</u> | 303 | | 327 |
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| <u>X95764</u> | 303 | | 327 |
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| <u>AF232022</u> | 400 | | 422 |
| <u>AF232021</u> | 400 | | 422 |
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| <u>AF118554</u> | 381 | | 403 |

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| <u>AF118549</u> | 381 | | 403 |
| <u>AF118548</u> | 381 | | 403 |
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| <u>AF326272</u> | 400 | | 422 |
| <u>AF326271</u> | 400 | | 422 |
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| <u>AF326266</u> | 400 | | 422 |
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| <u>AJ004264</u> | 302 |n..... | 326 |

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Gapped

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 39355

Number of Sequences: 807597

Number of extensions: 39355

Number of successful extensions: 15066

Number of sequences better than 10.0: 5706

length of query: 25

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 8

effective length of database: 2,850,098,736

effective search space: 22800789888

effective search space used: 22800789888

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

| | Score (bits) | E Value |
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| qb AF189111.1 AF189111 | 52 | 6e-06 |
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| qb AF123633.1 AF123633 | 52 | 6e-06 |
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| qb AF127194.1 AF127194 | 52 | 6e-06 |
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| qb AF160578.1 AF160578 | 52 | 6e-06 |
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| qb AF091629.1 AF091629 | 52 | 6e-06 |
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| qb AF038290.1 AF038290 | 52 | 6e-06 |
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| qb U81343.1 CFU81343 | 52 | 6e-06 |
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| qb M99464.1 PNZMTCYTB | 52 | 6e-06 |
| emb AJ225116.1 DNJ225116 | 52 | 6e-06 |
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| qb U25736.1 PRU25736 | 52 | 6e-06 |
| qb U15202.1 SMU15202 | 52 | 6e-06 |
| qb U15204.1 PRI5204 | 52 | 6e-06 |
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| emb X56286.1 MTAACYTBA | 52 | 6e-06 |
| dbj D88639.1 D88639 | 52 | 6e-06 |
| dbj D82890.1 D82890 | 52 | 6e-06 |
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| qb U62685.1 C9ICCYTB2 | 46 | 3e-04 |
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| emb AJ004229.1 SBAJ4229 | 46 | 3e-04 |
| emb AJ004232.1 SBAJ4232 | 46 | 3e-04 |
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| qb U90001.1 MBU90001 | 46 | 3e-04 |
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| dbj AB036402.1 AB036402 | 46 | 3e-04 |
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| gb AF082063.1 AF082063 | Elminia longicauda cytochrome b gene... | 44 | 0.001 |
| emb AJ010957.1 HAAJ10957 | Hippopotamus amphibius complete mi... | 44 | 0.001 |
| gb U76506.1 CLU76506 | Chlamydera lauterbachii cytochrome b g... | 44 | 0.001 |
| gb U76504.1 CCU76504 | Chlamydera cerviniventris cytochrome b... | 44 | 0.001 |
| gb U76505.1 ASU76505 | Amblyornis subalaris cytochrome b gene... | 44 | 0.001 |
| gb U76503.1 APU76503 | Archboldia papuensis cytochrome b gene... | 44 | 0.001 |
| gb U76508.1 AIU76508 | Amblyornis inornatus cytochrome b gene... | 44 | 0.001 |
| gb AF014969.1 AF014969 | Connochaetes taurinus cytochrome b g... | 44 | 0.001 |
| gb AF051876.1 AF051876 | Rhodeus ocellatus cytochrome b (cytb... | 44 | 0.001 |
| gb AF082007.1 AF082007 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082006.1 AF082006 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082005.1 AF082005 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082004.1 AF082004 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082003.1 AF082003 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082002.1 AF082002 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082001.1 AF082001 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF082000.1 AF082000 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081999.1 AF081999 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081998.1 AF081998 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081997.1 AF081997 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081996.1 AF081996 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081995.1 AF081995 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081994.1 AF081994 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081993.1 AF081993 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081992.1 AF081992 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081991.1 AF081991 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081990.1 AF081990 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081989.1 AF081989 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081988.1 AF081988 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081987.1 AF081987 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081986.1 AF081986 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081985.1 AF081985 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081984.1 AF081984 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081983.1 AF081983 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081982.1 AF081982 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081981.1 AF081981 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb AF081980.1 AF081980 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |

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| gb AF081991.1 AF081991 | Vireo plumbeus plumbeus specimen-vou... | 44 | 0.001 |
| gb S71150.1 S71150 | cytochrome b (Spermophilus richardsonii=... | 44 | 0.001 |
| gb AF012235.1 AF012235 | Cryptomys hottentotus natalensis cyt... | 44 | 0.001 |
| gb U53580.1 NCU53580 | Nycticebus coucang cytochrome b (cyt b... | 44 | 0.001 |
| gb U53577.1 EFU53577 | Eulemur fulvus rufus cytochrome b (cyt... | 44 | 0.001 |
| gb U53576.1 EFU53576 | Eulemur fulvus collaris cytochrome b (...) | 44 | 0.001 |
| gb U95512.1 ESERCYTB2 | Eptesicus serotinus 3' cytochrome b (...) | 44 | 0.001 |
| gb U95508.1 PKUHLCTB2 | Pipistrellus kuhli 5' cytochrome b (...) | 44 | 0.001 |
| gb U17868.1 BTU17868 | Budorcas taxicolor taxicolor cytochrom... | 44 | 0.001 |
| gb U17867.1 BTU17867 | Budorcas taxicolor bedfordi cytochrome... | 44 | 0.001 |
| gb U17860.1 ODU17860 | Ovis dalli cytochrome b gene, mitochon... | 44 | 0.001 |
| gb U17859.1 OCU17859 | Ovis canadensis cytochrome b gene, mit... | 44 | 0.001 |
| emb AJ010556.1 ASP010556 | Acomys spinosissimus mitochondrial... | 44 | 0.001 |
| gb AF034736.1 AF034736 | Capra falconeri cytochrome b (cytb) ... | 44 | 0.001 |
| gb AF034730.1 AF034730 | Ovis aries cytochrome b (cytb) gene, ... | 44 | 0.001 |
| gb AF034729.1 AF034729 | Ovis vignei cytochrome b (cytb) gene... | 44 | 0.001 |
| gb AF034728.1 | Ovis dalli dalli cytochrome b (cytb) gene, m... | 44 | 0.001 |
| gb AF034727.1 | Ovis ammon darwini cytochrome b (cytb) gene, ... | 44 | 0.001 |
| gb AF034724.1 AF034724 | Pantholops hodgsoni cytochrome b (cy... | 44 | 0.001 |
| gb AF034722.1 AF034722 | Addax nasomaculatus cytochrome b (cy... | 44 | 0.001 |
| gb U72038.1 MMU72038 | Monodon monoceros cytochrome b (cytb), ... | 44 | 0.001 |
| gb U72037.1 DLU72037 | Delphinapterus leucas cytochrome b (cy... | 44 | 0.001 |
| gb M99455.1 MUXMTCYTB | Murexia longicaudata cytochrome b gen... | 44 | 0.001 |
| gb L29055.1 SHEMTDLOOP | Sheep mitochondrial cytochrome b (Cy... | 44 | 0.001 |
| gb AF082047.1 AF082047 | Coccyzus americanus cytochrome b gen... | 44 | 0.001 |
| gb AF038286.1 AF038286 | Antechinus minimus cytochrome b gene... | 44 | 0.001 |
| gb AF038284.1 AF038284 | Antechinus swainsonii cytochrome b g... | 44 | 0.001 |
| gb AF059093.1 AF059093 | Anas undulata cytochrome b gene, par... | 44 | 0.001 |
| gb AF059092.1 AF059092 | Anas superciliosa rogersi cytochrome... | 44 | 0.001 |
| gb AF059091.1 AF059091 | Anas sparsa cytochrome b gene, parti... | 44 | 0.001 |
| gb AF059080.1 AF059080 | Anas melleri cytochrome b gene, part... | 44 | 0.001 |
| gb AF059078.1 AF059078 | Anas laysanensis cytochrome b gene, ... | 44 | 0.001 |
| gb AF052240.1 AF052240 | Anairetes flavirostris cytochrome b ... | 44 | 0.001 |
| gb AF006240.1 AF006240 | Mitrospingus cassinii cytochrome b (...) | 44 | 0.001 |
| gb AF006227.1 AF006227 | Dacnis cayana cytochrome b (cytb) ge... | 44 | 0.001 |
| gb AF047447.1 AF047447 | Oryx leucoryx cytochrome b gene, mit... | 44 | 0.001 |
| gb U07576.1 AHU07576 | Antechinus habbema mitochondrial cytoc... | 44 | 0.001 |
| gb AF028180.1 AF028180 | Urocyon cinereoargenteus cytochrome ... | 44 | 0.001 |
| gb AF028178.1 AF028178 | Pseudalopex sechurae cytochrome b (c... | 44 | 0.001 |
| gb AF028170.1 AF028170 | Vulpes zerda cytochrome b (cytb) gen... | 44 | 0.001 |
| gb M99454.1 ASWMTSCYTB | Antechinus stuartii cytochrome b gen... | 44 | 0.001 |
| gb M99453.1 ASWMTCYTB | Antechinus swainsonii cytochrome b ge... | 44 | 0.001 |
| gb U23461.1 ANU23461 | Antechinus naso cytochrome b gene, mit... | 44 | 0.001 |
| gb U87138.1 TVU87138 | Trichosurus vulpecula cytochrome b (cy... | 44 | 0.001 |
| gb U07590.1 PMU07590 | Planigale maculata mitochondrial cytoc... | 44 | 0.001 |
| emb AJ004326.1 PTAJ4326 | Phylloscopus trochilus mitochondria... | 44 | 0.001 |
| gb AF020255.1 AF020255 | Cyclura nubila cytochrome b (cytb) g... | 44 | 0.001 |
| emb Y19184.1 LPA19184 | Lama pacos complete mitochondrial genome | 44 | 0.001 |
| gb U88862.1 | Amphilophus citrinellum cytochrome b (cytb) ge... | 44 | 0.001 |
| gb U88859.1 | Thorichthys aureum cytochrome b (cytb) gene, m... | 44 | 0.001 |
| gb U88858.1 | Thorichthys cf. aureum cytochrome b (cytb) gen... | 44 | 0.001 |
| gb U88857.1 | Kerichthys labridens cytochrome b (cytb) gene, ... | 44 | 0.001 |
| gb U88856.1 | Kerichthys carpintis cytochrome b (cytb) gene, ... | 44 | 0.001 |
| emb Y10524.1 MIMRGEN | Macropus robustus complete mitochondri... | 44 | 0.001 |
| gb U81357.1 CSU81357 | Chelydra serpentina cytochrome b gene... | 44 | 0.001 |
| gb U81356.1 CLU81356 | Chelodina longicollis cytochrome b gen... | 44 | 0.001 |
| gb U75354.1 LUU75354 | Leptomermex unicolor cytochrome b gene... | 44 | 0.001 |
| gb U77332.1 GCU77332 | Gymnorhinus cyanocephala cytochrome-b ... | 44 | 0.001 |
| emb Z29571.1 QVMTGNME | Didelphis virginiana complete mitoch... | 44 | 0.001 |
| emb AJ222679.1 BTCYTQ8 | Soselaphus tragocamelus mitochondria... | 44 | 0.001 |
| emb AJ222680.1 TSCYTQ8 | Tragelaphus spekei mitochondrial cyt... | 44 | 0.001 |
| emb AJ222685.1 ODCYTQ8 | Oryx dammah mitochondrial cytochrome... | 44 | 0.001 |
| gb M22466.1 PMLMTCYTB | Perameles nasuta cytochrome b gene, c... | 44 | 0.001 |
| gb M22453.1 THVMTCYTB | Thylacinus cynocephalus cytochrome b... | 44 | 0.001 |
| gb M22450.1 DAVMTCYTB | Dasyurus hallucatus cytochrome b gene... | 44 | 0.001 |
| gb U25737.1 PMU25737 | Paradisea minor cytochrome b gene, ml... | 44 | 0.001 |
| gb U15203.1 PRU15203 | Paradisea rudolphi mitochondrial cyto... | 44 | 0.001 |
| gb U15205.1 PAU15205 | Eplimachus albertii mitochondrial cyto... | 44 | 0.001 |
| gb U15209.1 PRU15209 | Oliphilodes reepublica mitochondrial c... | 44 | 0.001 |
| emb AJ000424.1 STA424 | Sorex tundrensis partial mitochondrial... | 44 | 0.001 |
| emb AJ000423.1 STA423 | Sorex tundrensis partial mitochondrial... | 44 | 0.001 |

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| emb AJ000438.1 SIAJ438 | Sorex isodon partial mitochondrial c... | 44 | 0.001 |
| emb AJ000437.1 SIAJ437 | Sorex isodon partial mitochondrial c... | 44 | 0.001 |
| emb AJ000428.1 SAAJ428 | Sorex arcticus partial mitochondrial... | 44 | 0.001 |
| emb AJ000427.1 SAAJ427 | Sorex arcticus ssp. maritimensis par... | 44 | 0.001 |
| emb AJ000426.1 SAAJ426 | Sorex asper partial mitochondrial cy... | 44 | 0.001 |
| emb AJ000425.1 SAAJ425 | Sorex asper partial mitochondrial cy... | 44 | 0.001 |
| emb AJ000418.1 SGAJ418 | Sorex granarius partial mitochondria... | 44 | 0.001 |
| emb AJ000417.1 SGAJ417 | Sorex granarius partial mitochondria... | 44 | 0.001 |
| emb AJ000416.1 SAAJ416 | Sorex araneus partial mitochondrial ... | 44 | 0.001 |
| emb AJ004793.1 HCAJ4793 | Hippolais caligata ssp. caligata mi... | 44 | 0.001 |
| emb AJ004792.1 HCAJ4792 | Hippolais caligata ssp. rama mitoch... | 44 | 0.001 |
| gb U15718.1 RSU15718 | Ramphocelus sanguinolentus cytochrome ... | 44 | 0.001 |
| gb L11905.1 CGYMTCYTB0 | Cratogeomys gymnurus mitochondrial c... | 44 | 0.001 |
| gb U14679.1 POU14679 | Philander opossum cytochrome b light s... | 44 | 0.001 |
| gb L11907.1 CGYMTCYTB3 | Cratogeomys goldmani rubellus mitoch... | 44 | 0.001 |
| gb L11906.1 CGYMTCYTB2 | Cratogeomys merriami mitochondrial c... | 44 | 0.001 |
| gb L11902.1 CGYMTCYTB1 | Cratogeomys castanops castanops mito... | 44 | 0.001 |
| emb X92524.1 SLCYTB | S.longirostris cytochrome b gene (compl... | 44 | 0.001 |
| gb U46771.1 ACU46771 | Anthus campestris cytochrome b gene, m... | 44 | 0.001 |
| dbj AB021773.1 AB021773 | Anguilla interioris mitochondrial c... | 44 | 0.001 |
| dbj AB006953.1 AB006953 | Carassius auratus langsdorfi mitoch... | 44 | 0.001 |
| emb Z73492.1 MTPTTCYTB | P.trochilus mitochondrial cytochrome... | 44 | 0.001 |
| dbj AB035239.1 AB035239 | Osteoglossum ferreirai mitochondria... | 44 | 0.001 |
| emb X92532.1 MMCYTB2 | M.monoceros cytochrome b gene (complet... | 44 | 0.001 |
| emb X74260.1 MIVOCYTB | V.olivaceus mitochondrion gene for cy... | 44 | 0.001 |
| emb X56293.1 MISLCYTB3 | S.longirostris mitochondrion cytb gen... | 44 | 0.001 |
| emb X56292.1 MISLCYTB1 | S.longirostris mitochondrion cytb ge... | 44 | 0.001 |
| emb X74256.1 MIPVCYTB | P.violaceus mitochondrion gene for cy... | 44 | 0.001 |
| emb X82304.1 MIPHCYTB3 | P.hispida mitochondrial cytochrome b... | 44 | 0.001 |
| emb X82302.1 MIPFCYTB3 | P.fasciata mitochondrial cytochrome ... | 44 | 0.001 |
| emb X56284.1 MIOACYTB | O.aries mitochondrion cytb gene for c... | 44 | 0.001 |
| emb X74252.1 MIMKCYTB | M.keraudrenii mitochondrion gene for ... | 44 | 0.001 |
| emb X72005.1 MILWCYTB | L.weddelli mitochondrial gene for cyt... | 44 | 0.001 |
| emb X74259.1 MILLCYTB | L.ludovicianus mitochondrion gene for... | 44 | 0.001 |
| emb Y08814.1 MIHLCYTB3 | H.liberiensis mitochondrial cytochro... | 44 | 0.001 |
| emb Y08813.1 MIHACYTB | H.amphibius mitochondrial cytochrome ... | 44 | 0.001 |
| emb X56287.1 MIGCCYTB | G.camelopardalis mitochondrion cytb g... | 44 | 0.001 |
| emb X74253.1 MIEFCYTB | E.fastuosus mitochondrion gene for cy... | 44 | 0.001 |
| emb X60941.1 MIEACB33 | Epimachus albertisii mitochondrial ge... | 44 | 0.001 |
| emb X74255.1 MIDMCYTB | D.magnificus mitochondrion gene for c... | 44 | 0.001 |
| emb X56289.1 MICHCYTB | C.hircus mitochondrion cytb gene for ... | 44 | 0.001 |
| emb V00654.1 MISTXX | Bos taurus complete mitochondrial genome | 44 | 0.001 |
| emb X60940.1 MIAMCB33 | A.macgregoriae mitochondrial gene for... | 44 | 0.001 |
| emb X92530.1 LACYTB | L.albistrostris cytochrome b gene (comple... | 44 | 0.001 |
| gb U09265.1 CAU09265 | Coccyzus americanus mitochondrion cyto... | 44 | 0.001 |
| dbj AB023906.1 AB023906 | Petaurista leucogenys mitochondrial... | 44 | 0.001 |
| dbj AB023905.1 AB023905 | Petaurista leucogenys mitochondrial... | 44 | 0.001 |
| dbj AB023904.1 AB023904 | Petaurista leucogenys mitochondrial... | 44 | 0.001 |
| dbj AB023903.1 AB023903 | Petaurista leucogenys mitochondrial... | 44 | 0.001 |
| dbj D88981.1 D88981 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88638.1 D88638 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88636.1 D88636 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88635.1 D88635 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88633.1 D88633 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88632.1 D88632 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88630.1 D88630 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88628.1 D88628 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88627.1 D88627 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D84204.1 GOTMTCB0 | Capra aegagrus mitochondrial DNA for ... | 44 | 0.001 |
| dbj D84202.1 GOTMTCB8 | Capra falconeri mitochondrial DNA for... | 44 | 0.001 |
| dbj D82893.1 D82893 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D82892.1 D82892 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D82891.1 D82891 | Bos javanicus mitochondrial DNA for cyt... | 44 | 0.001 |
| dbj Q12121.1 BBUMTCB2 | Bubalus arnee bubalis mitochondrial ... | 44 | 0.001 |
| dbj Q14537.1 BBUMTCB1 | Bubalus bubalis mitochondrial gene fo... | 44 | 0.001 |
| dbj AB094974.1 AB094974 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| dbj AB094973.1 AB094973 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| dbj AB094972.1 AB094972 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| dbj AB094971.1 AB094971 | Capra aegagrus mitochondrial DNA fo... | 44 | 0.001 |
| dbj AB094970.1 AB094970 | Capra aegagrus mitochondrial DNA fo... | 44 | 0.001 |
| dbj D88549.1 D88549 | Anoa depressicornis mitochondrial DNA f... | 44 | 0.001 |
| dbj D88537.1 D88537 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |

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| dbj D88634.1 D88634 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88631.1 D88631 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D88629.1 D88629 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D84205.1 SHPMTCBE | Sheep mitochondrial DNA for cytochrom... | 44 | 0.001 |
| dbj D84203.1 SHPMTCBC | Ovis musimon mitochondrial DNA for cy... | 44 | 0.001 |
| dbj D84201.1 GOTMTCBA | Goat mitochondrial DNA for cytochrome... | 44 | 0.001 |
| dbj D82894.1 D82894 | Bubalus bubalis mitochondrial DNA for c... | 44 | 0.001 |
| dbj D82891.1 D82891 | Bubalus quarlesi mitochondrial DNA for ... | 44 | 0.001 |
| dbj D14638.1 BBUMTCBB | Bubalus bubalis mitochondrial gene fo... | 44 | 0.001 |
| dbj D14616.1 BOVMTCBB | Bos javanicus mitochondrial gene for ... | 44 | 0.001 |
| dbj AB017602.1 AB017602 | Talpa altaica mitochondrial cytb ge... | 44 | 0.001 |
| dbj AB018985.1 AB018985 | Cichlasoma citrinellum mitochondria... | 44 | 0.001 |
| dbj AB004075.1 AB004075 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| dbj AB004073.1 AB004073 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| dbj AB004070.1 AB004070 | Capra hircus mitochondrial DNA for ... | 44 | 0.001 |
| emb X92531.1 DLCYTB | D.leucas cytochrome b gene (complete se... | 44 | 0.001 |
| gb U07565.1 HAU07565 | Hippopotamus amphibius mitochondrion c... | 44 | 0.001 |
| gb U10367.1 PVU10367 | Ptilonorhynchus violaceus mitochondrio... | 44 | 0.001 |
| gb U10364.1 CMU10364 | Chlamydera maculata mitochondrion cyto... | 44 | 0.001 |
| emb Z96068.1 ASZ96068 | Acomys spinosissimus DNA for mitochon... | 42 | 0.005 |
| gb U76507.1 AIU76507 | Amblyornis inornatus cytochrome b gene... | 40 | 0.021 |
| gb AF157466.1 AF157466 | Lepus timidus cytochrome b (Cyb) gen... | 40 | 0.021 |
| gb AF157464.1 AF157464 | Lepus corsicanus haplotype 1 cytochr... | 40 | 0.021 |
| gb AF157463.1 AF157463 | Lepus corsicanus haplotype 3 cytochr... | 40 | 0.021 |
| gb AY016019.1 AY016018S3 | Mullerornis agilis cytochrome b ge... | 40 | 0.021 |
| gb AF027330.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027329.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027328.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027327.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027326.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027325.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027324.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027323.1 | Akodon olivaceus canescens museum catalog nu... | 40 | 0.021 |
| gb AF027322.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027321.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027320.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027319.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027318.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027317.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027316.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027315.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027314.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027313.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027312.1 | Akodon olivaceus beatus museum catalog numbe... | 40 | 0.021 |
| gb AF027311.1 | Akodon olivaceus brachiotis museum catalog n... | 40 | 0.021 |
| gb AF027310.1 | Akodon olivaceus brachiotis museum catalog n... | 40 | 0.021 |
| gb AF027309.1 | Akodon olivaceus brachiotis museum catalog n... | 40 | 0.021 |
| gb AF027308.1 | Akodon olivaceus brachiotis museum catalog n... | 40 | 0.021 |
| gb AF027307.1 | Akodon olivaceus brachiotis museum catalog n... | 40 | 0.021 |
| gb AF266188.1 AF266188 | Gillichthys mirabilis cytochrome b m... | 40 | 0.021 |
| gb AF324034.1 AF324034 | Phyllobates aurotaenia isolate Quebr... | 40 | 0.021 |
| gb AF272639.1 AF272639 | Clethrionomys gapperi specimen-vouch... | 40 | 0.021 |
| gb AF272636.1 AF272636 | Clethrionomys gapperi specimen-vouch... | 40 | 0.021 |
| gb AF272634.1 AF272634 | Clethrionomys gapperi specimen-vouch... | 40 | 0.021 |
| gb AF272633.1 AF272633 | Clethrionomys gapperi specimen-vouch... | 40 | 0.021 |
| gb AF182711.1 AF182711 | Geopelia cuneata cytochrome b gene. ... | 40 | 0.021 |
| gb AF182687.1 AF182687 | Columbina picui cytochrome b gene. p... | 40 | 0.021 |
| gb AF155422.1 AF155422 | Sigmodon ochrognathus cytochrome b (... | 40 | 0.021 |
| gb AF155400.1 AF155400 | Peromyscus pectoralis laceianus cyto... | 40 | 0.021 |
| gb AF155385.1 AF155385 | Peromyscus attwateri isolate 1b cyto... | 40 | 0.021 |
| gb AF155384.1 AF155384 | Peromyscus attwateri isolate 1a cyto... | 40 | 0.021 |
| gb AF155522.1 AF155522 | Sigmodon ochrognathus isolate Af12AC... | 40 | 0.021 |
| gb AF155521.1 AF155521 | Sigmodon ochrognathus isolate Mc11v7... | 40 | 0.021 |
| gb AF155520.1 AF155520 | Sigmodon ochrognathus isolate Duran4... | 40 | 0.021 |
| gb AF155519.1 AF155519 | Sigmodon ochrognathus isolate El-Mt8... | 40 | 0.021 |
| gb AF155518.1 AF155518 | Sigmodon ochrognathus isolate Bb-end4... | 40 | 0.021 |
| gb AF133531.1 AF133531 | Trachyphonus darnaudii cytochrome b ... | 40 | 0.021 |
| gb AF254947.1 AF254947 | Urocyon vancouverensis cytochrome b gene. co... | 40 | 0.021 |
| gb AF205511.1 AF205511 | Podarcis sicula cytochrome b gene. p... | 40 | 0.021 |
| gb AF123705.1 AF123705 | Hippocampus zosterae haplotype PK.14... | 40 | 0.021 |
| ccl NC 009994.1 | Cavia porcellus complete mitochondrial genome | 42 | 0.021 |

| | | | |
|--------------------------------|---|-----------|-------|
| <u>gb AF004572.1 AF004572</u> | Arvicanthus niloticus cytochrome b (...) | <u>40</u> | 0.021 |
| <u>gb AF088932.1 AF088932</u> | Sminthopsis psammophila cytochrome b... | <u>40</u> | 0.021 |
| <u>gb U62697.1 ORUCYTB2</u> | Oreopholus ruficollis cytochrome b (cy... | <u>40</u> | 0.021 |
| <u>gb U62681.1 CACYTB2</u> | Charadrius australis cytochrome b (cyt ...) | <u>40</u> | 0.021 |
| <u>gb U62707.1 CVERCYTB2</u> | Charadrius veredus cytochrome b (cytb... | <u>38</u> | 0.084 |
| <u>emb AJ004315.1 HCAJ4315</u> | Hippolais caligata mitochondrial cy... | <u>38</u> | 0.084 |

Alignments

| | | | |
|-----------------|-------|-----------------------------|-------|
| tmpseq_0 | 1 | cctccctagttctgtagggattgatcg | 26 |
| <u>AF189111</u> | 797 | | 772 |
| <u>U86834</u> | 858 | | 833 |
| <u>AF123633</u> | 56 | | 31 |
| <u>AF123617</u> | 104 | | 79 |
| <u>AF127202</u> | 107 | | 82 |
| <u>AF127194</u> | 107 | | 82 |
| <u>AF217828</u> | 845 | | 820 |
| <u>AF160578</u> | 869 | | 844 |
| <u>AF009931</u> | 869 | | 844 |
| <u>AF091629</u> | 869 | | 844 |
| <u>AF034967</u> | 869 | | 844 |
| <u>AF038290</u> | 869 | | 844 |
| <u>U07577</u> | 869 | | 844 |
| <u>U81343</u> | 791 | | 766 |
| <u>AJ222681</u> | 869 | | 844 |
| <u>M99464</u> | 869 | | 844 |
| <u>AJ225116</u> | 869 | | 844 |
| <u>U25738</u> | 872 | | 847 |
| <u>U25736</u> | 872 | | 847 |
| <u>U15202</u> | 872 | | 847 |
| <u>U15204</u> | 872 | | 847 |
| <u>X56290</u> | 869 | | 844 |
| <u>X56286</u> | 869 | | 844 |
| <u>D88639</u> | 869 | | 844 |
| <u>D82890</u> | 869 | | 844 |
| <u>AF119261</u> | 869 | | 847 |
| <u>AF123615</u> | 101 | | 79 |
| <u>AF160603</u> | 866 | | 844 |
| <u>U62687</u> | 179 | | 157 |
| <u>U62685</u> | 179 | | 157 |
| <u>AF022071</u> | 866 | | 844 |
| <u>AF022070</u> | 866 | | 844 |
| <u>U83317</u> | 872 | | 850 |
| <u>U37293</u> | 774 | | 752 |
| <u>U37292</u> | 774 | | 752 |
| <u>U37291</u> | 774 | | 752 |
| <u>AF082055</u> | 51 | | 29 |
| <u>U72770</u> | 798 | | 776 |
| <u>U07578</u> | 869 | | 847 |
| <u>AF011908</u> | 187 | | 165 |
| <u>AJ004231</u> | 773 | | 751 |
| <u>AJ004230</u> | 773 | | 751 |
| <u>AJ004229</u> | 773 | | 751 |
| <u>AJ004232</u> | 773 | | 751 |
| <u>U88865</u> | 850 | | 828 |
| <u>U90001</u> | 536 | | 514 |
| <u>U63057</u> | 773 | | 751 |
| <u>AB016404</u> | 173 | | 151 |
| <u>AB016402</u> | 173 | | 151 |
| <u>AB016400</u> | 173 | | 151 |
| <u>AB016398</u> | 173 | | 151 |
| <u>U19611</u> | 774 | | 752 |
| <u>X22519</u> | 869 | | 847 |
| <u>L08014</u> | 872 | | 850 |
| <u>L08011</u> | 872 | | 850 |
| <u>AX016012</u> | 11937 | | 11912 |
| <u>AF074591</u> | 677 | | 652 |
| <u>AX005212</u> | 761 | | 736 |
| <u>AX005211</u> | 761 | | 736 |
| <u>AF189133</u> | 797 | | 772 |
| <u>AF189120</u> | 797 | | 772 |

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|------------------|-------|-------------|-------|
| <u>AF189118</u> | 797 |a..... | 772 |
| <u>AF189117</u> | 797 |a..... | 772 |
| <u>AF189116</u> | 797 |g..... | 772 |
| <u>AF112140</u> | 310 |g..... | 285 |
| <u>AF112139</u> | 310 |g..... | 285 |
| <u>AF112138</u> | 310 |g..... | 285 |
| <u>AF081990</u> | 872 |c..... | 847 |
| <u>AF081989</u> | 872 |c..... | 847 |
| <u>AF081988</u> | 872 |c..... | 847 |
| <u>AF081987</u> | 872 |c..... | 847 |
| <u>AF081986</u> | 872 |c..... | 847 |
| <u>AF081985</u> | 872 |c..... | 847 |
| <u>AF081984</u> | 872 |c..... | 847 |
| <u>AF081983</u> | 872 |c..... | 847 |
| <u>AF081982</u> | 872 |c..... | 847 |
| <u>AF081981</u> | 872 |c..... | 847 |
| <u>AF081980</u> | 872 |c..... | 847 |
| <u>AF081979</u> | 872 |c..... | 847 |
| <u>AF081978</u> | 872 |c..... | 847 |
| <u>AF081977</u> | 872 |c..... | 847 |
| <u>AF081976</u> | 872 |c..... | 847 |
| <u>AF081975</u> | 872 |c..... | 847 |
| <u>AF081974</u> | 872 |c..... | 847 |
| <u>AF081973</u> | 872 |c..... | 847 |
| <u>AF081972</u> | 872 |c..... | 847 |
| <u>AF081971</u> | 872 |c..... | 847 |
| <u>AF081970</u> | 872 |c..... | 847 |
| <u>AF081969</u> | 872 |c..... | 847 |
| <u>AF081968</u> | 872 |c..... | 847 |
| <u>AF081967</u> | 872 |c..... | 847 |
| <u>AF081966</u> | 872 |c..... | 847 |
| <u>AF081965</u> | 872 |c..... | 847 |
| <u>AF081964</u> | 872 |c..... | 847 |
| <u>AF081962</u> | 754 |c..... | 729 |
| <u>AF081961</u> | 872 |c..... | 847 |
| <u>AF081960</u> | 872 |g..... | 847 |
| <u>AF081959</u> | 872 |c..... | 847 |
| <u>AF112405</u> | 869 |c..... | 844 |
| <u>AF144317</u> | 161 |g..... | 136 |
| <u>AF144316</u> | 161 |g..... | 136 |
| <u>AF144315</u> | 161 |g..... | 136 |
| <u>AF144314</u> | 161 |g..... | 136 |
| <u>AF144313</u> | 161 |g..... | 136 |
| <u>AF144312</u> | 161 |g..... | 136 |
| <u>AF144311</u> | 161 |g..... | 136 |
| <u>AF144310</u> | 161 |g..... | 136 |
| <u>AF144309</u> | 161 |g..... | 136 |
| <u>NC 001567</u> | 15382 |g..... | 15357 |
| <u>AF212124</u> | 425 |c..... | 400 |
| <u>AF182706</u> | 739 |a..... | 714 |
| <u>AF010406</u> | 15027 |a..... | 15002 |
| <u>AF096452</u> | 735 |c..... | 710 |
| <u>AF281619</u> | 845 |a..... | 820 |
| <u>AF281618</u> | 845 |a..... | 820 |
| <u>AF281608</u> | 845 |a..... | 820 |
| <u>AF281602</u> | 845 |a..... | 820 |
| <u>AF310062</u> | 770 |a..... | 745 |
| <u>AF146616</u> | 95 |g..... | 70 |
| <u>AF271410</u> | 869 |g..... | 844 |
| <u>AF290132</u> | 752 |g..... | 727 |
| <u>NC 002504</u> | 15022 |g..... | 14997 |
| <u>AF161901</u> | 869 |g..... | 844 |
| <u>AF119261</u> | 869 |g..... | 844 |
| <u>AF119259</u> | 869 |g..... | 844 |
| <u>AF288454</u> | 91 |a..... | 66 |
| <u>AF161829</u> | 869 |c..... | 844 |
| <u>AF121642</u> | 68 |g..... | 43 |
| <u>AF121647</u> | 68 |g..... | 43 |
| <u>AF121646</u> | 104 |g..... | 77 |
| <u>AF121645</u> | 68 |g..... | 43 |
| <u>AF121644</u> | 84 |g..... | 59 |

| | | | |
|------------------|-------|-------------|-------|
| <u>AF123628</u> | 104 |g..... | 79 |
| <u>AF123621</u> | 85 |g..... | 60 |
| <u>AF123619</u> | 104 |g..... | 79 |
| <u>AF123618</u> | 104 |g..... | 79 |
| <u>AF123614</u> | 104 |g..... | 79 |
| <u>AF123613</u> | 101 |g..... | 76 |
| <u>AF127201</u> | 107 |g..... | 82 |
| <u>AF127192</u> | 107 |c..... | 82 |
| <u>AF127189</u> | 107 |g..... | 82 |
| <u>AF197849</u> | 872 |g..... | 847 |
| <u>AF197847</u> | 872 |c..... | 847 |
| <u>NC 000889</u> | 15040 |g..... | 15015 |
| <u>NC 002079</u> | 16164 |g..... | 16139 |
| <u>NC 001794</u> | 15052 |a..... | 15027 |
| <u>NC 001610</u> | 15045 |c..... | 15020 |
| <u>AF201612</u> | 520 |c..... | 495 |
| <u>AF097931</u> | 869 |a..... | 844 |
| <u>AF097927</u> | 869 |g..... | 844 |
| <u>J01394</u> | 15382 |g..... | 15357 |
| <u>AF168760</u> | 507 |a..... | 482 |
| <u>AF168759</u> | 507 |a..... | 482 |
| <u>AF168758</u> | 507 |a..... | 482 |
| <u>AF168756</u> | 507 |a..... | 482 |
| <u>AF182381</u> | 692 |c..... | 667 |
| <u>AF182380</u> | 692 |c..... | 667 |
| <u>U89187</u> | 872 |a..... | 847 |
| <u>AF193833</u> | 773 |g..... | 748 |
| <u>AF193822</u> | 773 |g..... | 748 |
| <u>AF193821</u> | 773 |a..... | 748 |
| <u>AF217837</u> | 845 |c..... | 820 |
| <u>AF217835</u> | 845 |c..... | 820 |
| <u>AF217834</u> | 845 |a..... | 820 |
| <u>AF217831</u> | 845 |g..... | 820 |
| <u>AF217823</u> | 845 |a..... | 820 |
| <u>AF217819</u> | 845 |a..... | 820 |
| <u>AF217815</u> | 845 |c..... | 820 |
| <u>AF118156</u> | 101 |g..... | 76 |
| <u>AF209938</u> | 418 |a..... | 393 |
| <u>AF209933</u> | 418 |a..... | 393 |
| <u>AF059104</u> | 776 |c..... | 751 |
| <u>AF059102</u> | 776 |c..... | 751 |
| <u>AF059054</u> | 776 |c..... | 751 |
| <u>AF192646</u> | 869 |c..... | 844 |
| <u>AF192645</u> | 869 |c..... | 844 |
| <u>AF160614</u> | 869 |g..... | 844 |
| <u>AF160613</u> | 869 |g..... | 844 |
| <u>AF160612</u> | 869 |g..... | 844 |
| <u>AF160611</u> | 238 |g..... | 213 |
| <u>AF160610</u> | 869 |g..... | 844 |
| <u>AF160604</u> | 869 |g..... | 844 |
| <u>AF160560</u> | 869 |a..... | 844 |
| <u>AF160559</u> | 869 |a..... | 844 |
| <u>AF160558</u> | 869 |a..... | 844 |
| <u>AF160557</u> | 869 |a..... | 844 |
| <u>AF160555</u> | 869 |a..... | 844 |
| <u>AF160554</u> | 869 |a..... | 844 |
| <u>AF160553</u> | 869 |a..... | 844 |
| <u>AF160552</u> | 869 |a..... | 844 |
| <u>AF160551</u> | 869 |a..... | 844 |
| <u>AF160550</u> | 869 |a..... | 844 |
| <u>AF160549</u> | 869 |a..... | 844 |
| <u>AFQ16287</u> | 869 |g..... | 844 |
| <u>AFQ16286</u> | 869 |g..... | 844 |
| <u>AFQ16281</u> | 869 |a..... | 844 |
| <u>AFQ16281</u> | 869 |a..... | 844 |
| <u>AFQ16278</u> | 869 |g..... | 844 |
| <u>AFQ16276</u> | 867 |a..... | 844 |
| <u>AFQ16274</u> | 869 |g..... | 844 |
| <u>NC 001794</u> | 15027 |a..... | 15002 |
| <u>AF198628</u> | 869 |a..... | 844 |

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|-----------------|-------|-------------|-------|
| <u>AF108682</u> | 869 |a..... | 844 |
| <u>AF108673</u> | 869 |g..... | 844 |
| <u>AF108669</u> | 857 |g..... | 832 |
| <u>AF042720</u> | 869 |a..... | 844 |
| <u>AF042718</u> | 869 |a..... | 844 |
| <u>AF084082</u> | 869 |a..... | 844 |
| <u>AF084081</u> | 869 |a..... | 844 |
| <u>AF084074</u> | 869 |a..... | 844 |
| <u>AF090750</u> | 869 |a..... | 844 |
| <u>AF157939</u> | 869 |a..... | 844 |
| <u>AF157937</u> | 869 |a..... | 844 |
| <u>AF157936</u> | 869 |a..... | 844 |
| <u>AF157915</u> | 869 |a..... | 844 |
| <u>AF157914</u> | 869 |a..... | 844 |
| <u>AF157912</u> | 869 |g..... | 844 |
| <u>AF157906</u> | 869 |g..... | 844 |
| <u>AF157891</u> | 869 |g..... | 844 |
| <u>AF157882</u> | 869 |a..... | 844 |
| <u>AF157859</u> | 869 |a..... | 844 |
| <u>AF157858</u> | 869 |a..... | 844 |
| <u>AF157839</u> | 869 |g..... | 844 |
| <u>AF030497</u> | 50 |a..... | 25 |
| <u>U03541</u> | 869 |g..... | 844 |
| <u>AF009951</u> | 866 |a..... | 841 |
| <u>AF009941</u> | 869 |g..... | 844 |
| <u>AF009925</u> | 869 |a..... | 844 |
| <u>AF094633</u> | 737 |g..... | 712 |
| <u>AF094621</u> | 737 |c..... | 712 |
| <u>AF094618</u> | 737 |c..... | 712 |
| <u>AF166348</u> | 869 |g..... | 844 |
| <u>AF158697</u> | 869 |a..... | 844 |
| <u>AF158694</u> | 869 |a..... | 844 |
| <u>AF158693</u> | 869 |a..... | 844 |
| <u>AF158688</u> | 869 |a..... | 844 |
| <u>AF100720</u> | 869 |a..... | 844 |
| <u>AF091632</u> | 869 |a..... | 844 |
| <u>AF102815</u> | 869 |a..... | 844 |
| <u>AF102814</u> | 869 |c..... | 844 |
| <u>AF022065</u> | 869 |a..... | 844 |
| <u>AF022059</u> | 869 |g..... | 844 |
| <u>AF022058</u> | 869 |a..... | 844 |
| <u>AF022057</u> | 869 |g..... | 844 |
| <u>AF022054</u> | 869 |a..... | 844 |
| <u>AF016637</u> | 869 |c..... | 844 |
| <u>U69863</u> | 845 |c..... | 820 |
| <u>U69844</u> | 845 |c..... | 820 |
| <u>AF143193</u> | 869 |a..... | 844 |
| <u>AF121222</u> | 140 |g..... | 115 |
| <u>AF096625</u> | 869 |g..... | 844 |
| <u>AF096624</u> | 869 |g..... | 844 |
| <u>AF081052</u> | 869 |a..... | 844 |
| <u>AF081049</u> | 869 |a..... | 844 |
| <u>AF081048</u> | 869 |g..... | 844 |
| <u>AF082063</u> | 54 |g..... | 29 |
| <u>AJ010957</u> | 15040 |g..... | 15015 |
| <u>U76506</u> | 773 |g..... | 748 |
| <u>U76504</u> | 773 |g..... | 748 |
| <u>U76505</u> | 773 |c..... | 748 |
| <u>U76503</u> | 773 |c..... | 748 |
| <u>U76508</u> | 773 |c..... | 748 |
| <u>AF034969</u> | 869 |g..... | 844 |
| <u>AF051876</u> | 869 |c..... | 844 |
| <u>AF082007</u> | 872 |c..... | 847 |
| <u>AF082006</u> | 872 |c..... | 847 |
| <u>AF082005</u> | 872 |c..... | 847 |
| <u>AF082004</u> | 872 |c..... | 847 |
| <u>AF082003</u> | 872 |c..... | 847 |
| <u>AF082002</u> | 872 |c..... | 847 |
| <u>AF082001</u> | 872 |c..... | 847 |
| <u>AF082000</u> | 872 |c..... | 847 |
| <u>AF081999</u> | 872 |c..... | 847 |
| <u>AF081998</u> | 872 |c..... | 847 |

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|-----------------|-------|-------------|-------|
| <u>AF081998</u> | 872 |t..... | 847 |
| <u>AF081997</u> | 872 |t..... | 847 |
| <u>AF081996</u> | 872 |t..... | 847 |
| <u>AF081995</u> | 872 |t..... | 847 |
| <u>AF081994</u> | 872 |t..... | 847 |
| <u>AF081993</u> | 872 |t..... | 847 |
| <u>AF081992</u> | 872 |t..... | 847 |
| <u>AF081991</u> | 872 |t..... | 847 |
| <u>S73150</u> | 869 |a..... | 844 |
| <u>AF012235</u> | 860 |a..... | 835 |
| <u>U53580</u> | 869 |g..... | 844 |
| <u>U53577</u> | 869 |g..... | 844 |
| <u>U53576</u> | 869 |a..... | 844 |
| <u>U95512</u> | 31 |g..... | 6 |
| <u>U95508</u> | 31 |a..... | 6 |
| <u>U17868</u> | 869 |g..... | 844 |
| <u>U17867</u> | 869 |g..... | 844 |
| <u>U17860</u> | 869 |g..... | 844 |
| <u>U17859</u> | 800 |g..... | 775 |
| <u>AJ010556</u> | 869 |g..... | 844 |
| <u>AF034736</u> | 869 |g..... | 844 |
| <u>AF034730</u> | 869 |a..... | 844 |
| <u>AF034729</u> | 869 |a..... | 844 |
| <u>AF034728</u> | 869 |g..... | 844 |
| <u>AF034727</u> | 869 |a..... | 844 |
| <u>AF034724</u> | 869 |g..... | 844 |
| <u>AF034722</u> | 869 |g..... | 844 |
| <u>U72038</u> | 869 |g..... | 844 |
| <u>U72037</u> | 869 |g..... | 844 |
| <u>M99455</u> | 869 |a..... | 844 |
| <u>L29055</u> | 260 |a..... | 235 |
| <u>AF082047</u> | 54 |g..... | 29 |
| <u>AF038286</u> | 869 |t..... | 844 |
| <u>AF038284</u> | 869 |t..... | 844 |
| <u>AF059093</u> | 776 |t..... | 751 |
| <u>AF059092</u> | 776 |t..... | 751 |
| <u>AF059091</u> | 776 |t..... | 751 |
| <u>AF059080</u> | 776 |t..... | 751 |
| <u>AF059078</u> | 776 |t..... | 751 |
| <u>AF052240</u> | 61 |a..... | 36 |
| <u>AF006240</u> | 774 |t..... | 749 |
| <u>AF006227</u> | 774 |g..... | 749 |
| <u>AF047447</u> | 41 |g..... | 16 |
| <u>U07576</u> | 869 |g..... | 844 |
| <u>AF028180</u> | 65 |g..... | 40 |
| <u>AF028178</u> | 69 |g..... | 44 |
| <u>AF028170</u> | 77 |g..... | 52 |
| <u>M99454</u> | 869 |a..... | 844 |
| <u>M99451</u> | 869 |t..... | 844 |
| <u>U23461</u> | 869 |c..... | 844 |
| <u>U87138</u> | 869 |g..... | 844 |
| <u>U07590</u> | 869 |g..... | 844 |
| <u>A7004226</u> | 773 |c..... | 748 |
| <u>AF020255</u> | 819 |g..... | 794 |
| <u>Y19184</u> | 15022 |g..... | 14997 |
| <u>U88862</u> | 843 |a..... | 818 |
| <u>U88859</u> | 867 |g..... | 842 |
| <u>U88858</u> | 843 |c..... | 818 |
| <u>U88857</u> | 863 |g..... | 838 |
| <u>U88856</u> | 867 |g..... | 842 |
| <u>Y10534</u> | 15052 |a..... | 15027 |
| <u>U81357</u> | 791 |t..... | 766 |
| <u>U81356</u> | 791 |a..... | 766 |
| <u>U75354</u> | 452 |a..... | 427 |
| <u>U77332</u> | 872 |g..... | 847 |
| <u>Z29571</u> | 15045 |t..... | 15020 |
| <u>AJ223679</u> | 869 |g..... | 844 |
| <u>AJ222680</u> | 869 |a..... | 844 |
| <u>AJ222681</u> | 869 |g..... | 844 |
| <u>M99468</u> | 869 |a..... | 844 |
| <u>M99432</u> | 869 |c..... | 844 |

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|------------------|-------|-------------|-------|
| <u>M99460</u> | 869 |g..... | 844 |
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| <u>X74256</u> | 872 |g..... | 847 |
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| <u>X82302</u> | 869 |g..... | 844 |
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| <u>X74252</u> | 872 |g..... | 847 |
| <u>X72005</u> | 869 |g..... | 844 |
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| <u>Q12121</u> | 869 |a..... | 844 |

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| <u>AF027307</u> | 869 | | 850 |
| <u>AF266188</u> | 371 | | 352 |
| <u>AF324034</u> | 408 | | 389 |
| <u>AF272639</u> | 869 | | 850 |
| <u>AF272636</u> | 869 | | 850 |
| <u>AF272634</u> | 869 | | 850 |
| <u>AF272631</u> | 869 | | 850 |
| <u>AF182711</u> | 712 | | 693 |
| <u>AF182687</u> | 774 | | 755 |
| <u>AF155422</u> | 869 | | 850 |
| <u>AF155400</u> | 869 | | 850 |
| <u>AF155385</u> | 869 | | 850 |
| <u>AF155384</u> | 869 | | 850 |
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| <u>AF155391</u> | 869 | | 850 |
| <u>AF155390</u> | 869 | | 850 |

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| <u>AF155588</u> | 869 | | 850 |
| <u>AF123531</u> | 771 | | 752 |
| <u>AF264047</u> | 869 | | 850 |
| <u>AF206531</u> | 771 | | 752 |
| <u>AF192706</u> | 863 | | 844 |
| <u>NC 000884</u> | 15032 | | 15013 |
| <u>AF004572</u> | 869 | | 850 |
| <u>AF088932</u> | 869 | | 850 |
| <u>U62697</u> | 176 | | 157 |
| <u>U62681</u> | 179 | | 160 |
| <u>U62707</u> | 179 |g.....n.. | 154 |
| <u>AJ004315</u> | 773 |t.....n..... | 748 |

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Gapped

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

| SN. | Name of the animal |
|-----|------------------------|
| 1. | Indian black buck no.1 |
| 2. | Indian black buck no 2 |
| 3 | sheep |
| 4 | pig |
| 5 | dog |
| 6 | chimpanzee (chimss) |
| 7 | human (humsk) |
| 8 | Hamster |
| 9 | crocodile no1 |
| 10 | crocodile no2 |
| 11 | turtle no1 |
| 12 | turtle no2 |
| 13 | mouse |
| 14 | varanus |
| 15 | Naga-naga snake |
| 16 | Indian elephant |
| 17 | hen |
| 18 | dugong |
| 19 | lizard |
| 20 | weaver bird no1 |
| 21 | weaver bird no2 |
| 22 | buffalo no1 |
| 23 | buffalo no 2 |

CLAIMS

- 1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

| primers name | Sequence (5'-3') |
|--------------|-----------------------------|
| mcb 398 | "TACCATGAGGACAAATATCATTCTG" |
| mcb 869 | "CCTCCTAGTTTGTAGGGATTGATCG" |

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:
- Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:
- "taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcggtacaaacctag tagaatgaatctgaggagggttctcagtagataaagcaaccctacccgattttcgcttccactttatctcccatttatcattgc agcccttaccatagtagacactactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaa attccattccacccctactacactatcaaagatatacctaggagctctactattaattttaaccctcatgcttctagtcctatttcacc ggacctgcttgagagaccagacaactatacaccagcaaaccacttaatacaccacacatatcaagcccgaatgatacttc ctatttgcatagcgaatcctccgatcaattcctaacaaactaggagg"
6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
 - sequencing the amplified products,
 - blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- 5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- 10 g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal
- 15 of the biological sample.
7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 20 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 μ l reaction volume containing approximately 20 ng of template DNA, 100 μ M each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95^oC for 10 min, followed by 35 cycles each of denaturation at 95^oC for 45 s, annealing at 51^oC for 1 min, and extension at 72^oC for 2 min. The extension step at 35th cycles should be held for 10 min.
- 25 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 30 10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

- 5 12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
- 15 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 20 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECULAR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.

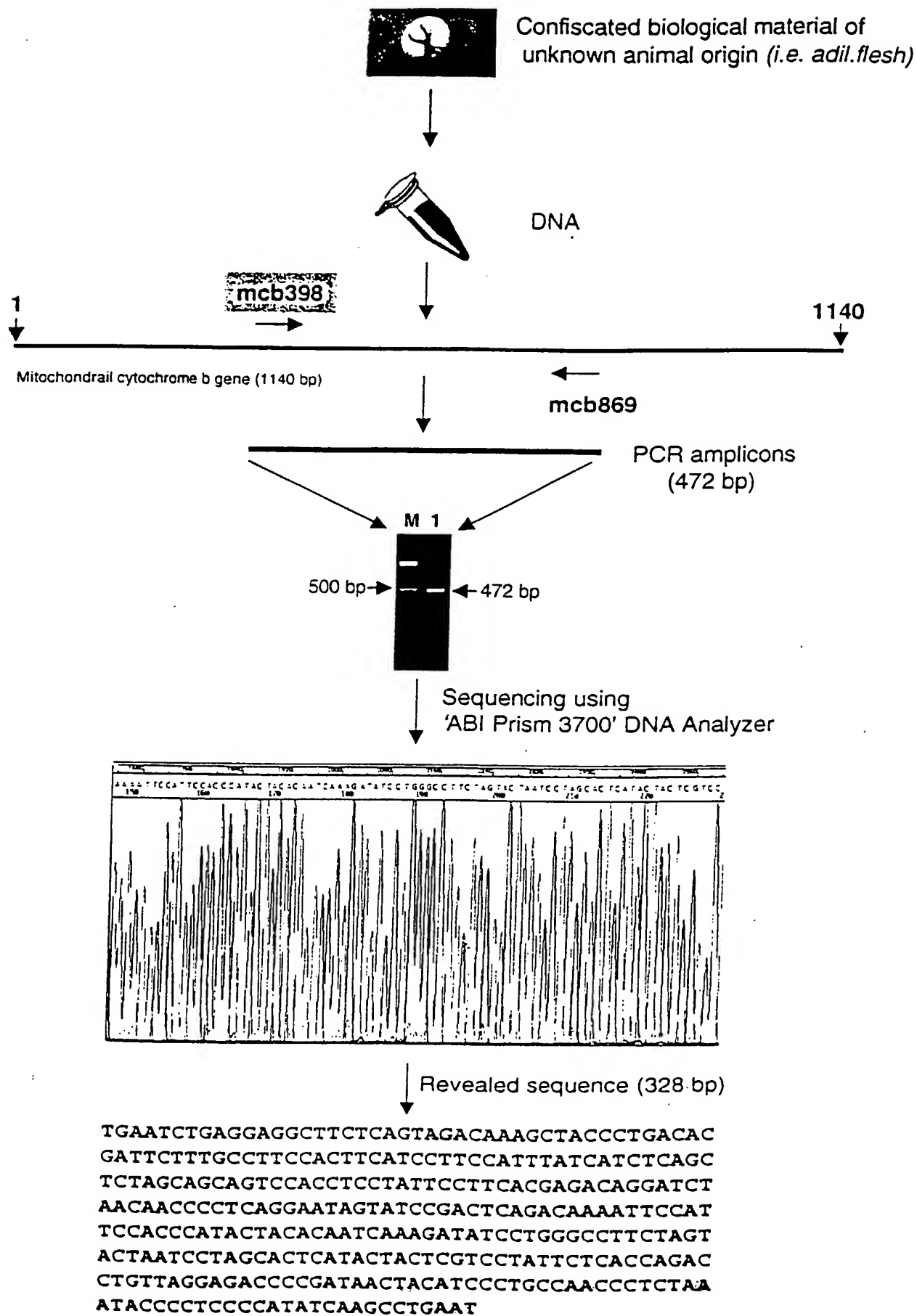
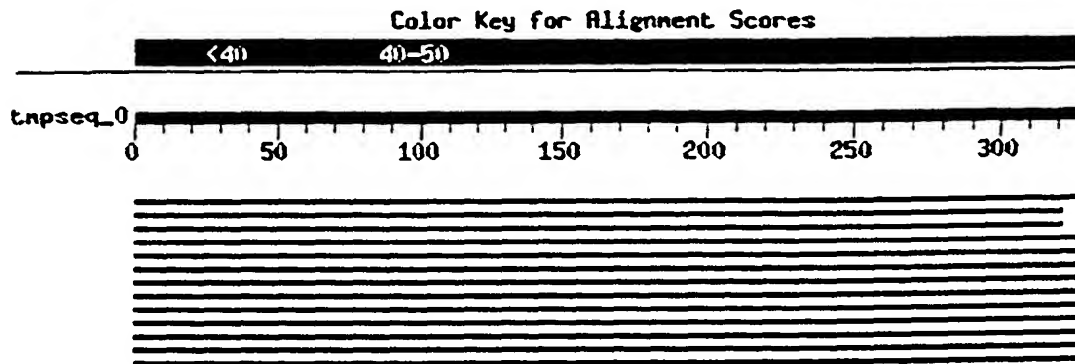


Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers 'mcb398' and 'mcb869'

Homology search in '*nr*' database using '*BLAST*'

<http://www.ncbi.nlm.nih.gov/BLAST/>



| Sequences producing significant alignments: | Score (bits) | E Value |
|---|-----------------|------------|
| gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c... | 603 | e-170 |
| gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1... | 527 | e-147 |
| gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi... | 527 | e-147 |
| gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ... | 476 | e-132 |
| gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ... | 476 | e-132 |

Selection of reference animals based on above information
and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments
using '*Autoassembler*'

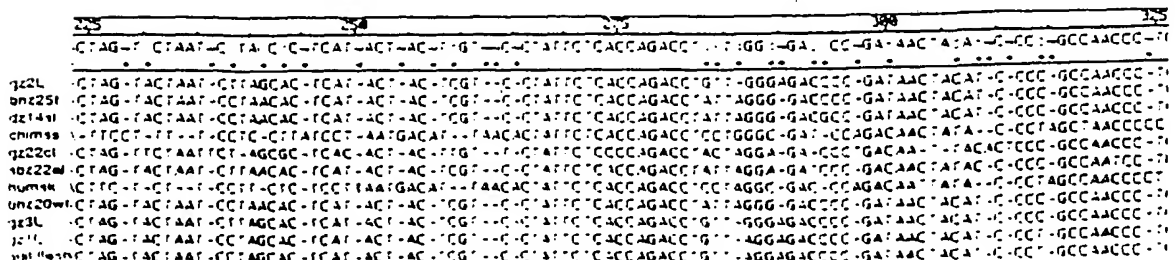


Figure 1 b

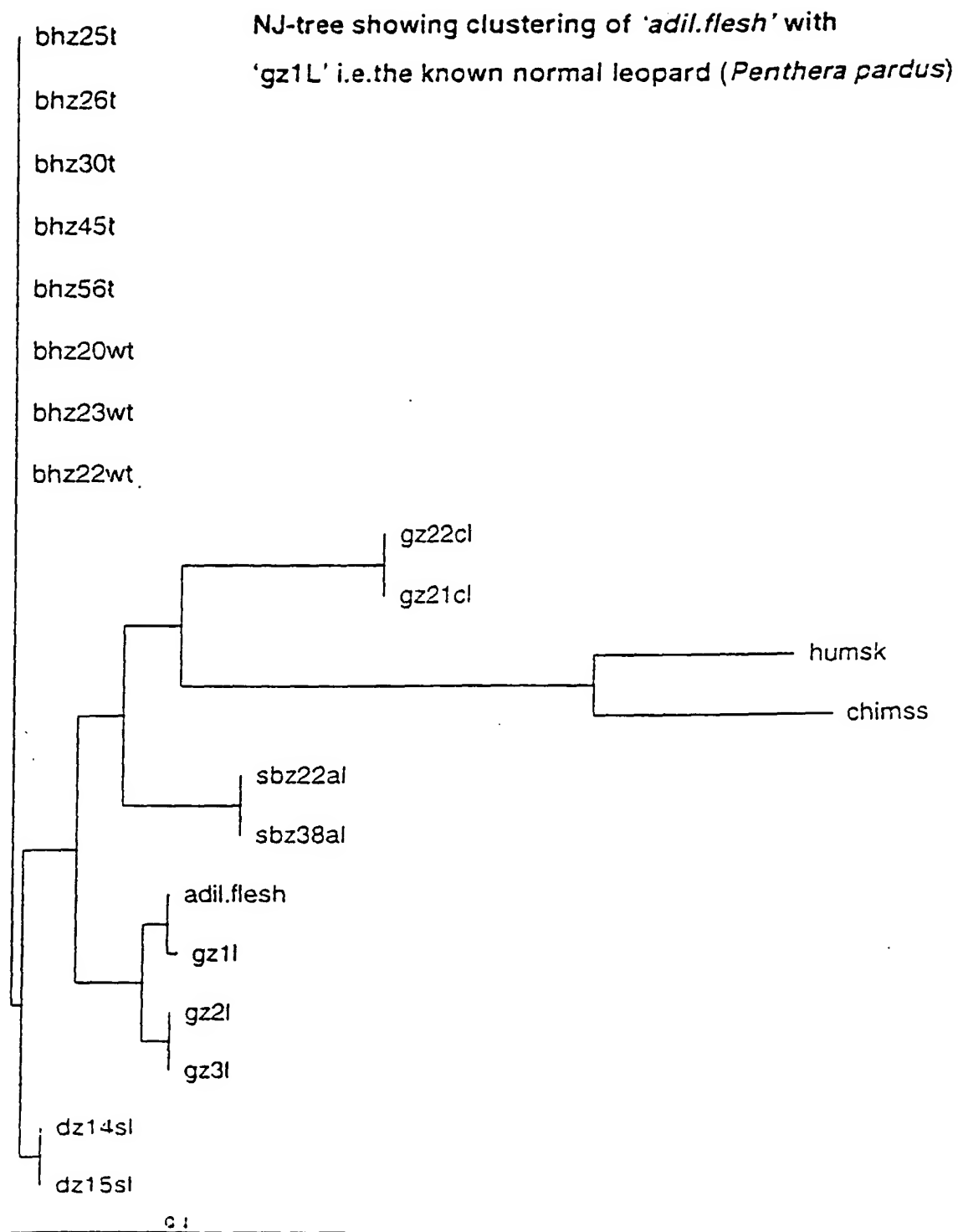


Figure 1c

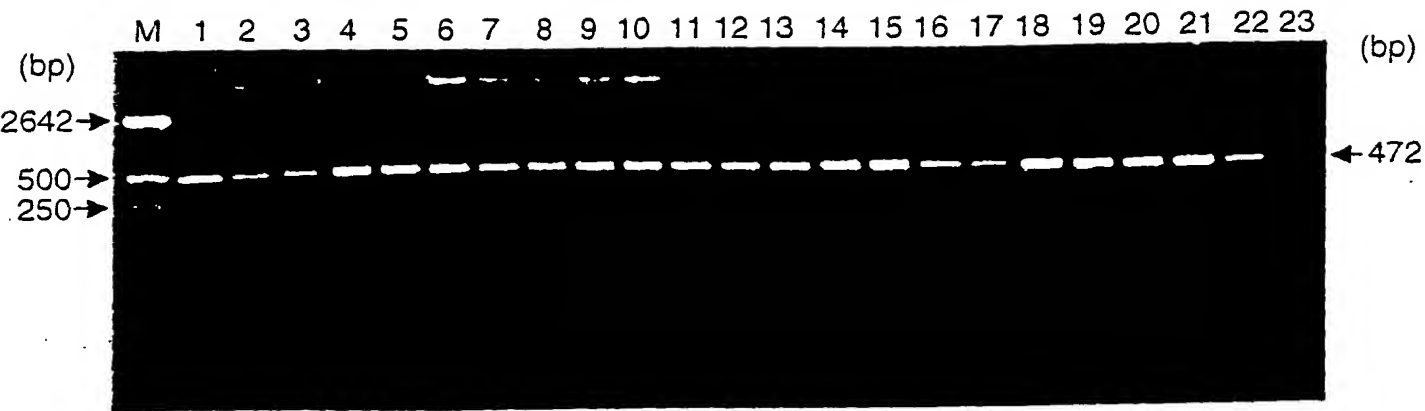


Figure 2

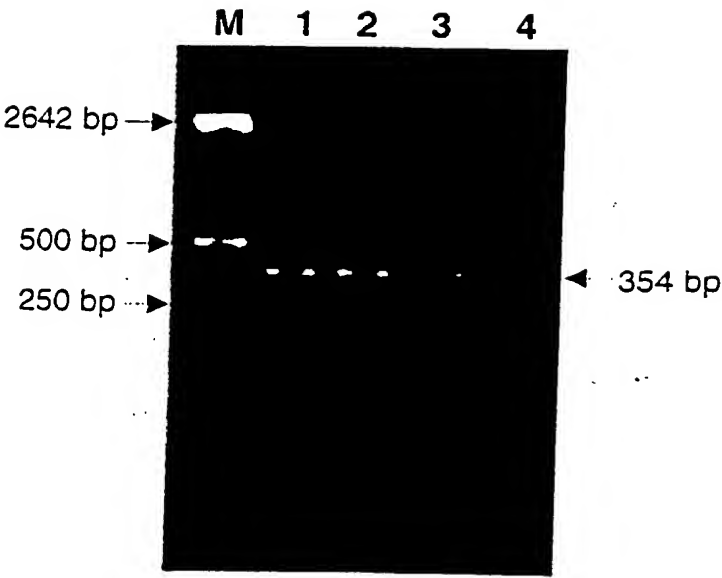


Figure 3

6/6



Figure 4

INTERNATIONAL SEARCH REPORT

Inte Application No
PC 1 / 1 IN 01/00055

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

° Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
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- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

12/03/2002

Name and mailing address of the ISA

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Authorized officer

Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IN 01/00055

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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Int. Application No

PCT/JP 01/00055

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| | | | DK 550491 T3 | 24-07-1995 |
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